

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Mizzen, Lee
Wisniewski, Jan
- (ii) TITLE OF INVENTION: STREPTOCACCAL HEAT SHOCK PROTEINS OF THE
HSP60 FAMILY
- (iii) NUMBER OF SEQUENCES: 91
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 701 Fifth Avenue, 6300 Columbia Center
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/001,737
 - (B) FILING DATE: 31-DEC-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sharkey, Richard G.
 - (B) REGISTRATION NUMBER: 32,629
 - (C) REFERENCE/DOCKET NUMBER: 870109.408
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-5031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1649
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCT TCAT ATG GCG GCT AAA GAC GTA AAA TTC GGT AAC GAC GCT 50
Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala
1 5 10

CGT GTG AAA ATG CTG CGC GGC GTA AAC GTA CTG GCA GAT GCA GTG AAA 98
Arg Val Lys Met Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys
15 20 25

GTT ACC CTC GGC CCA AAA GGC CGT AAC GTA GTT CTG GAT AAA TCT TTC 146
Val Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe
30 35 40

GGT GCA CCG ACC ATC ACT AAA GAT GGT GTT TCC GTA GCA CGT GAA ATC 194
Gly Ala Pro Thr Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile
45 50 55 60

GAA CTG GAA GAC AAG TTC GAA AAC ATG GGT GCG CAG ATG GTG AAA GAA 242
Glu Leu Glu Asp Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu
65 70 75

GTT GCC TCT AAA GCG AAC GAC GCT GCA GGT GAC GGT ACC ACC ACC GCA 290
Val Ala Ser Lys Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala
80 85 90

ACC GTA CTG GCT CAG TCC ATC ATC ACT GAA GGC CTG AAA GCC GTT GCT 338
Thr Val Leu Ala Gln Ser Ile Ile Thr Glu Gly Leu Lys Ala Val Ala
95 100 105

CGC GGC ATG AAC CCG ATG GAT CTG AAA CGT GGT ATC GAC AAA GCT GTC 386
Ala Gly Met Asn Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val
110 115 120

GCT GCT GCT GTT GAA GAA CTG AAA GCA CTG TCC GTA CCG TGC TCC GAC 434
Ala Ala Ala Val Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp
125 130 135 140

TCT AAA GCT ATT GCT CAG GTT GGT ACC ATC TCC GCT AAC TCC GAC GAA 482
Ser Lys Ala Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu
145 150 155

ACC GTA GGT AAA CTG ATC GCT GAA GCG ATG GAC AAA GTC GGT AAA GAA 530
Thr Val Gly Lys Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu
160 165 170

GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG CAG GAC GAA CTG GAC 578
Gly Val Ile Thr Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp
175 180 185

GTG GTT GAA GGT ATG CAG TTC GAC CGT GGC TAC CTG TCT CCT TAC TTC 626
Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe
190 195 200

ATC AAC AAG CCG GAA ACT GGC GCA GTA GAA TTG GAA AGC CCG TTC ATC 674
Ile Asn Lys Pro Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile
205 210 215 220

CTG CTG GCT GAC AAG AAA ATC TCC AAC ATC CGC GAA ATG CTG CCG GTT 722

Leu Leu Ala Asp Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val
225 230 235

CTG GAA GCT GTA GCG AAA GCA GGC AAA CCG CTG CTG ATC ATC GCT GAA 770
Leu Glu Ala Val Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu
240 245 250

GAT GTT GAA GGC GAA GCG CTG GCA ACT CTG GTT GTT AAC ACC ATG CGC 818
Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg
255 260 265

GGT ATC GTA AAA GTC GCT GCG GTT AAA GCA CCT GGC TTC GGC GAT CGT 866
Gly Ile Val Lys Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg
270 275 280

CGT AAA GCA ATG CTG CAG GAT ATC GCT ACC CTG ACC GGT GGT ACC GTT 914
Arg Lys Ala Met Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val
285 290 295 300

ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCA ACT CTG GAA GAT 962
Ile Ser Glu Glu Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp
305 310 315

CTG GGC CAG GCG AAA CGC GTT GTT ATC AAC AAA GAT ACC ACC ACC ATC 1010
Leu Gly Gln Ala Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile
320 325 330

ATC GAT GGC GTG GGC GAC GAA GCT GCA ATC CAG GGT CGC GTG ACT CAG 1058
Ile Asp Gly Val Gly Asp Glu Ala Ala Ile Gln Gly Arg Val Thr Gln
335 340 345

ATT CGT CAG CAG ATC GAA GAA GCA ACT TCC GAC TAT GAC CGT GAA AAA 1106
Ile Arg Gln Gln Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys
350 355 360

CTG CAG GAG CGC GTA GCG AAA CTG GCA GGC GGC GTT GCG GTT ATC AAA 1154
Leu Gln Glu Arg Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys
365 370 375 380

GTT GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAG AAA GCC CGC GTT 1202
Val Gly Ala Ala Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val
385 390 395

GAA GAT GCC CTG CAC GCT ACC CGT GCT GCG GTA GAA GAA GGC GTG GTT 1250
Glu Asp Ala Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val
400 405 410

GCT GGT GGT GGC GTT GCG CTG ATT CGC GTA GCG TCT AAA ATT GCC GGC 1298
Ala Gly Gly Gly Val Ala Leu Ile Arg Val Ala Ser Lys Ile Ala Gly
415 420 425

CTG AAA GGT CAG AAC GAA GAC CAG AAC GTA GGT ATC AAA GTT GCG CTG 1346
Leu Lys Gly Gln Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu
430 435 440

CGC GCA ATG GAA TCC CCA CTG CGT CAA ATC GTA CTG AAC TGC GGC GAA 1394
Arg Ala Met Glu Ser Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu
445 450 455 460

GAG CCG TCT GTA GTG GCT AAC ACC GTG AAA GCC GGT GAC GGT AAC TAC	1442
Glu Pro Ser Val Val Ala Asn Thr Val Lys Ala Gly Asp Gly Asn Tyr	
465 470 475	
GGT TAC AAC GCT GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC ATG GGT	1490
Gly Tyr Asn Ala Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly	
480 485 490	
ATC CTG GAT CCA ACC AAA GTA ACT CGT TCT GCT CTG CAG TAC GCG GCT	1538
Ile Leu Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala	
495 500 505	
TCT GTT GCG GGT CTG ATG ATC ACC ACC GAG TGC ATG GTT ACC GAC CTG	1586
Ser Val Ala Gly Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu	
510 515 520	
CCG AAA GGC GAT GCA CCT GAC TTA GGT GCT GCT GGT GGT ATG GGC GGC	1634
Pro Lys Gly Asp Ala Pro Asp Leu Gly Ala Ala Gly Gly Met Gly Gly	
525 530 535 540	
ATG GGC GGA ATG ATG TGATCAAGCC GAATTC	1665
Met Gly Gly Met Met	
545	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met	
1 5 10 15	
Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly	
20 25 30	
Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr	
35 40 45	
Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp	
50 55 60	
Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys	
65 70 75 80	
Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala	
85 90 95	
Gln Ser Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn	
100 105 110	

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Ala Ala Ala Val
 115 120 125
 Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
 130 135 140
 Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
 145 150 155 160
 Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
 165 170 175
 Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
 180 185 190
 Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
 195 200 205
 Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
 210 215 220
 Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
 225 230 235 240
 Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
 245 250 255
 Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
 260 265 270
 Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
 275 280 285
 Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
 290 295 300
 Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala
 305 310 315 320
 Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
 325 330 335
 Gly Asp Glu Ala Ala Ile Gln Gly Arg Val Thr Gln Ile Arg Gln Gln
 340 345 350
 Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
 355 360 365
 Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
 370 375 380
 Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu
 385 390 395 400
 His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
 405 410 415
 Val Ala Leu Ile Arg Val Ala Ser Lys Ile Ala Gly Leu Lys Gly Gln

420 425 430
 Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu
 435 440 445
 Ser Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val
 450 455 460
 Val Ala Asn Thr Val Lys Ala Gly Asp Gly Asn Tyr Gly Tyr Asn Ala
 465 470 475 480
 Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro
 485 490 495
 Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly
 500 505 510
 Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Gly Asp
 515 520 525
 Ala Pro Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met
 530 535 540
 Met
 545

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCT TCAT ATG GCA AAA GAA ATT AAA TTT TCA TCA GAT GCC CGT 50
 Met Ala Lys Glu Ile Lys Phe Ser Ser Asp Ala Arg
 1 5 10
 TCA GCT ATG GTC CGT GGT GTC GAT ATC CTT GCA GAT ACT GTT AAA GTA 98
 Ser Ala Met Val Arg Gly Val Asp Ile Leu Ala Asp Thr Val Lys Val
 15 20 25
 ACT TTG GGA CCA AAA GGT CGC AAT GTC GTT CTT GAA AAG TCA TTC GGT 146
 Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Ser Phe Gly
 30 35 40
 TCA CCC TTG ATT ACC AAT GAC GGT GTG ACT ATT GCC AAA GAA ATT GAA 194
 Ser Pro Leu Ile Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu
 45 50 55 60

TTA GAA GAC CAT TTT GAA AAT ATG GGT GCC AAA TTG GTA TCA GAA GTA	242
Leu Glu Asp His Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val	
65 70 75	
GCT TCA AAA ACC AAT GAT ATC GCA GGT GAT GGA ACT ACA ACT GCA ACT	290
Ala Ser Lys Thr Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr	
80 85 90	
GTT TTG ACC CAA GCA ATC GTC CGT GAA GGA ATC AAA AAC GTC ACA GCA	338
Val Leu Thr Gln Ala Ile Val Arg Glu Gly Ile Lys Asn Val Thr Ala	
95 100 105	
GGT GCA AAT CCA ATC GGT ATT CGT CGT GGG ATT GAA ACA GCA GTT GCC	386
Gly Ala Asn Pro Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Val Ala	
110 115 120	
GCA GCA GTT GAA GCT TTG AAA AAC AAC GTC ATC CCT GTT GCC AAT AAA	434
Ala Ala Val Glu Ala Leu Lys Asn Asn Val Ile Pro Val Ala Asn Lys	
125 130 135 140	
GAA GCT ATC GCT CAA GTT GCA GCC GTA TCT TCT CGT TCT GAA AAA GTT	482
Glu Ala Ile Ala Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val	
145 150 155	
GGT GAG TAC ATC TCT GAA GCA ATG GAA AAA GTT GGC AAA GAC GGT GTC	530
Gly Glu Tyr Ile Ser Glu Ala Met Glu Lys Val Gly Lys Asp Gly Val	
160 165 170	
ATC ACC ATC GAA GAG TCA CGT GGT ATG GAA ACA GAG CTT GAA GTC GTA	578
Ile Thr Ile Glu Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val	
175 180 185	
GAA GGA ATG CAG TTT GAC CGT GGT TAC CTT TCA CAG TAC ATG GTG ACA	626
Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr	
190 195 200	
GAT AGC GAA AAA ATG GTG GCT GAC CTT GAA AAT CCG TAC ATT TTG ATT	674
Asp Ser Glu Lys Met Val Ala Asp Leu Glu Asn Pro Tyr Ile Leu Ile	
205 210 215 220	
ACA GAC AAG AAA ATT TCC AAT ATC CAA GAA ATC TTG CCA CTT TTG GAA	722
Thr Asp Lys Lys Ile Ser Asn Ile Gln Glu Ile Leu Pro Leu Leu Glu	
225 230 235	
AGC ATT CTC CAA AGC AAT CGT CCA CTC TTG ATT ATT GCG GAT GAT GTG	770
Ser Ile Leu Gln Ser Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val	
240 245 250	
GAT GGT GAG GCT CTT CCA ACT CTT GTT TTG AAC AAG ATT CGT GGA ACC	818
Asp Gly Glu Ala Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr	
255 260 265	
TTC AAC GTA GTA GCA GTC AAG GCA CCT GGT TTT GGT GAC CGT CGC AAA	866
Phe Asn Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys	
270 275 280	
GCC ATG CTT GAA GAT ATC GCC ATC TTA ACA GGC GGA ACA GTT ATC ACA	914

Ala Met Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Thr	
285 290 295 300	
GAA GAC CTT GGT CTT GAG TTG AAA GAT GCG ACA ATT GAA GCT CTT GGT	962
Glu Asp Leu Gly Leu Glu Leu Lys Asp Ala Thr Ile Glu Ala Leu Gly	
305 310 315	
CAA GCA GCG AGA GTG ACC GTG GAC AAA GAT AGC ACG GTT ATT GTA GAA	1010
Gln Ala Ala Arg Val Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu	
320 325 330	
GGT GCA GGA AAT CCT GAA GCG ATT TCT CAC CGT GTT GCG GTT ATC AAG	1058
Gly Ala Gly Asn Pro Glu Ala Ile Ser His Arg Val Ala Val Ile Lys	
335 340 345	
TCT CAA ATC GAA ACT ACA ACT TCT GAA TTT GAC CGT GAA AAA TTG CAA	1106
Ser Gln Ile Glu Thr Thr Thr Ser Glu Phe Asp Arg Glu Lys Leu Gln	
350 355 360	
GAA CGC TTG GCC AAA TTG TCA GGT GGT GTA GCG GTT ATT AAG GTC GGA	1154
Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly	
365 370 375 380	
GCC GCA ACT GAA ACT GAG TTG AAA GAA ATG AAA CTC CGC ATT GAA GAT	1202
Ala Ala Thr Glu Thr Glu Leu Lys Glu Met Lys Leu Arg Ile Glu Asp	
385 390 395	
GCC CTC AAC GCT ACT CGT GCA GCT GTT GAA GAA GGT ATT GTT GCA GGT	1250
Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly	
400 405 410	
GGT GGA ACA GCT CTT GCC AAT GTG ATT CCA GCT GTT GCT ACC TTG GAA	1298
Gly Gly Thr Ala Leu Ala Asn Val Ile Pro Ala Val Ala Thr Leu Glu	
415 420 425	
TTG ACA GGA GAT GAA GCA ACA GGA CGT AAT ATT GTT CTC CGT GCT TTG	1346
Leu Thr Gly Asp Glu Ala Thr Gly Arg Asn Ile Val Leu Arg Ala Leu	
430 435 440	
GAA GAA CCT GTT CGT CAA ATT GCT CAC AAT GCA GGA TTT GAA GGA TCT	1394
Glu Glu Pro Val Arg Gln Ile Ala His Asn Ala Gly Phe Glu Gly Ser	
445 450 455 460	
ATC GTT ATC GAT CGT TTG AAA AAT GCT GAG CTT GGT ATA GGA TTC AAC	1442
Ile Val Ile Asp Arg Leu Lys Asn Ala Glu Leu Gly Ile Gly Phe Asn	
465 470 475	
GCA GCA ACT GGC GAG TGG GTT AAC ATG ATT GAT CAA GGT ATC ATT GAT	1490
Ala Ala Thr Gly Glu Trp Val Asn Met Ile Asp Gln Gly Ile Ile Asp	
480 485 490	
CCA GTT AAA GTG AGT CGT TCA GCC CTA CAA AAT GCA GCA TCT GTA GCC	1538
Pro Val Lys Val Ser Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala	
495 500 505	
AGC TTG ATT TTG ACA ACA GAA GCA GTC GTA GCC AAT AAA CCA GAA CCA	1586
Ser Leu Ile Leu Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro	
510 515 520	

GTA GCC CCA GCT CCA GCA ATG GAT CCA AGT ATG ATG GGT GGA ATG GGC 1634
 Val Ala Pro Ala Pro Ala Met Asp Pro Ser Met Met Gly Gly Met Gly
 525 530 535 540

GGA TGATCAAAGC CGAATTC 1654
 Gly

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Lys Glu Ile Lys Phe Ser Ser Asp Ala Arg Ser Ala Met Val
 1 5 10 15

Arg Gly Val Asp Ile Leu Ala Asp Thr Val Lys Val Thr Leu Gly Pro
 20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Ser Phe Gly Ser Pro Leu Ile
 35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His
 50 55 60

Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val Ala Ser Lys Thr
 65 70 75 80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Gln
 85 90 95

Ala Ile Val Arg Glu Gly Ile Lys Asn Val Thr Ala Gly Ala Asn Pro
 100 105 110

Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Val Ala Ala Val Glu
 115 120 125

Ala Leu Lys Asn Asn Val Ile Pro Val Ala Asn Lys Glu Ala Ile Ala
 130 135 140

Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val Gly Glu Tyr Ile
 145 150 155 160

Ser Glu Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Ile Glu
 165 170 175

Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val Glu Gly Met Gln
 180 185 190

Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr Asp Ser Glu Lys

195	200	205
Met Val Ala Asp Leu Glu Asn Pro Tyr Ile Leu Ile Thr Asp Lys Lys 210 215 220		
Ile Ser Asn Ile Gln Glu Ile Leu Pro Leu Leu Glu Ser Ile Leu Gln 225 230 235 240		
Ser Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val Asp Gly Glu Ala 245 250 255		
Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr Phe Asn Val Val 260 265 270		
Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Glu 275 280 285		
Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Thr Glu Asp Leu Gly 290 295 300		
Leu Glu Leu Lys Asp Ala Thr Ile Glu Ala Leu Gly Gln Ala Ala Arg 305 310 315 320		
Val Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu Gly Ala Gly Asn 325 330 335		
Pro Glu Ala Ile Ser His Arg Val Ala Val Ile Lys Ser Gln Ile Glu 340 345 350		
Thr Thr Thr Ser Glu Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365		
Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu 370 375 380		
Thr Glu Leu Lys Glu Met Lys Leu Arg Ile Glu Asp Ala Leu Asn Ala 385 390 395 400		
Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Thr Ala 405 410 415		
Leu Ala Asn Val Ile Pro Ala Val Ala Thr Leu Glu Leu Thr Gly Asp 420 425 430		
Glu Ala Thr Gly Arg Asn Ile Val Leu Arg Ala Leu Glu Glu Pro Val 435 440 445		
Arg Gln Ile Ala His Asn Ala Gly Phe Glu Gly Ser Ile Val Ile Asp 450 455 460		
Arg Leu Lys Asn Ala Glu Leu Gly Ile Gly Phe Asn Ala Ala Thr Gly 465 470 475 480		
Glu Trp Val Asn Met Ile Asp Gln Gly Ile Ile Asp Pro Val Lys Val 485 490 495		
Ser Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Ile Leu 500 505 510		

Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Val Ala Pro Ala
 515 520 525

Pro Ala Met Asp Pro Ser Met Met Gly Gly Met Gly Gly
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCT TCAT ATG GCG GCT AAA GAT GTA AAA TTC GGT AAC GAC GCT 50
 Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala
 1 5 10

CGT GTA AAA ATG CTC CGC GGC GTA AAC GTA CTG GCA GAC GCA GTT AAA 98
 Arg Val Lys Met Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys
 15 20 25

GTA ACC CTG GGC CCG AAA GGC CGT AAC GTA GTG CTG GAC AAA TCC TTC 146
 Val Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe
 30 35 40

GGC GCG CCA ACC ATC ACG AAA GAT GGT GTT TCT GTA GCA CGT GAA ATC 194
 Gly Ala Pro Thr Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile
 45 50 55 60

GAG CTG GAA GAC AAG TTC GAA AAC ATG GGC GCG CAG ATG GTG AAA GAA 242
 Glu Leu Glu Asp Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu
 65 70 75

GTG GCC TCT AAA GCG AAC GAC GCT GCA GGC GAC GGT ACC ACC ACC GCG 290
 Val Ala Ser Lys Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala
 80 85 90

ACC GTG CTG GCT CAG GCT ATC ATC ACC GAA GGT CTG AAA GCC GTT GCT 338
 Thr Val Leu Ala Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala
 95 100 105

GCG GGC ATG AAC CCA ATG GAT CTG AAA CGT GGT ATC GAC AAA GCT GTC 386
 Ala Gly Met Asn Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val
 110 115 120

GCG TCC GCT GTT GAA GAA CTG AAA GCG CTG TCC GTA CCG TGC TCT GAC 434
 Ala Ser Ala Val Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp

125	130	135	140	
TCT AAA GCC ATT GCT CAG GTA GGT ACC ATC TCC GCT AAC TCC GAC GAA Ser Lys Ala Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu	145	150	155	482
ACC GTA GGT AAA CTG ATC GCG GAA GCG ATG GAT AAA GTC GGT AAA GAA Thr Val Gly Lys Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu	160	165	170	530
GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG GAA GAC GAA CTG GAC Gly Val Ile Thr Val Glu Asp Gly Thr Gly Leu Glu Asp Glu Leu Asp	175	180	185	578
GTG GTT GAA GGT ATG CAG TTC GAC CGC GGT TAC CTG TCC CCA TAC TTC Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe	190	195	200	626
ATC AAC AAG CCA GAA ACT GGC GCT GTT GAG CTG GAA AGC CCG TTC ATC Ile Asn Lys Pro Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile	205	210	215	674
CTG CTG GCT GAC AAG AAA ATC TCC AAC ATC CGC GAA ATG CTG CCA GTG Leu Leu Ala Asp Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val	225	230	235	722
CTG GAA GCC GTT GCG AAA GCA GGC AAA CCG CTG GTT ATC ATT GCT GAA Leu Glu Ala Val Ala Lys Ala Gly Lys Pro Leu Val Ile Ile Ala Glu	240	245	250	770
GAC GTT GAA GGC GAA GCG CTG GCG ACC CTG GTG GTT AAC ACC ATG CGT Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg	255	260	265	818
GGC ATC GTG AAA GTG GCT GCG GTT AAA GCA CCT GGC TTC GGC GAC CGC Gly Ile Val Lys Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg	270	275	280	866
CGT AAA GCG ATG CTG CAG GAT ATC GCT ACC CTG ACC GGC GGT ACC GTC Arg Lys Ala Met Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val	285	290	295	914
ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCG ACC CTG GAA GAC Ile Ser Glu Glu Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp	305	310	315	962
CTG GGC CAG GCT AAA CGT GTT GTG ATC AAC AAA GAC ACC ACC ACC ATC Leu Gly Gln Ala Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile	320	325	330	1010
ATC GAT GGC GTG GGC GAC GAA GCG GCG ATT CAG GGC CGT GTT GGT CAG Ile Asp Gly Val Gly Asp Glu Ala Ala Ile Gln Gly Arg Val Gly Gln	335	340	345	1058
ATC CGT AAG CAG ATC GAA GAA GCC ACT TCC GAT TAC GAC CGT GAA AAA Ile Arg Lys Gln Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys	350	355	360	1106

CTG CAG GAG CGC GTA GCG AAA CTG GCA GGC GGT GTT GCG GTA ATC AAA Leu Gln Glu Arg Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys 365 370 375 380	1154
GTC GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAA AAA GCA CGC GTT Val Gly Ala Ala Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val 385 390 395	1202
GAC GAT GCC CTG CAC GCG ACC CGT GCT GCG GTA GAA GAA GGC GTG GTT Asp Asp Ala Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val 400 405 410	1250
GCT GGT GGT GGT GTG GCG CTG GTG CGT GTT GCC GCG AAA CTG TCC GGC Ala Gly Gly Gly Val Ala Leu Val Arg Val Ala Ala Lys Leu Ser Gly 415 420 425	1298
CTG ACT GCT CAG AAC GAA GAT CAG AAC GTG GGT ATC AAA GTT GCG CTG Leu Thr Ala Gln Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu 430 435 440	1346
GCG GCA ATG GAA GCT CCA CTG CGT CAG ATC GTG TCC AAC GCC GGT GAA Arg Ala Met Glu Ala Pro Leu Arg Gln Ile Val Ser Asn Ala Gly Glu 445 450 455 460	1394
GAG CCA TCT GTT GTG ACC AAC AAC GTG AAA GCA GGC GAA GGT AAC TAC Glu Pro Ser Val Val Thr Asn Asn Val Lys Ala Gly Glu Gly Asn Tyr 465 470 475	1442
GGT TAC AAC GCA GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC TTC GGT Gly Tyr Asn Ala Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Phe Gly 480 485 490	1490
ATC CTG GAT CCA ACC AAA GTG ACC CGT TCT GCT CTG CAG TAC GCG GCA Ile Leu Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala 495 500 505	1538
TCT GTC GCT GGC CTG ATG ATC ACC ACC GAG TGC ATG GTG ACC GAC CTG Ser Val Ala Gly Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu 510 515 520	1586
CCT AAA GGC GAC GCA CCT GAC TTA GGT GCT GCA GGC ATG GGT GGG ATG Pro Lys Gly Asp Ala Pro Asp Leu Gly Ala Ala Gly Met Gly Gly Met 525 530 535 540	1634
GGC GGT ATG ATG TGATCAAGCC GAATTC Gly Gly Met Met	1662

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met
1 5 10 15

Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
20 25 30

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
85 90 95

Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
100 105 110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Ala Ser Ala Val
115 120 125

Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
130 135 140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
145 150 155 160

Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
165 170 175

Val Glu Asp Gly Thr Gly Leu Glu Asp Glu Leu Asp Val Val Glu Gly
180 185 190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
195 200 205

Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
210 215 220

Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
225 230 235 240

Ala Lys Ala Gly Lys Pro Leu Val Ile Ile Ala Glu Asp Val Glu Gly
245 250 255

Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
260 265 270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
275 280 285

Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
290 295 300

Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala
 305 310 315 320
 Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
 325 330 335
 Gly Asp Glu Ala Ala Ile Gln Gly Arg Val Gly Gln Ile Arg Lys Gln
 340 345 350
 Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
 355 360 365
 Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
 370 375 380
 Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Asp Asp Ala Leu
 385 390 395 400
 His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
 405 410 415
 Val Ala Leu Val Arg Val Ala Ala Lys Leu Ser Gly Leu Thr Ala Gln
 420 425 430
 Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu
 435 440 445
 Ala Pro Leu Arg Gln Ile Val Ser Asn Ala Gly Glu Glu Pro Ser Val
 450 455 460
 Val Thr Asn Asn Val Lys Ala Gly Glu Gly Asn Tyr Gly Tyr Asn Ala
 465 470 475 480
 Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Phe Gly Ile Leu Asp Pro
 485 490 495
 Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly
 500 505 510
 Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Gly Asp
 515 520 525
 Ala Pro Asp Leu Gly Ala Ala Gly Met Gly Gly Met Gly Gly Met Met
 530 535 540

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 15..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCT TCAT ATG GCA AAA GAA ATC AAA TTT TCA GCA GAT GCG CGT 50
Met Ala Lys Glu Ile Lys Phe Ser Ala Asp Ala Arg
1 5 10

GCT GCC ATG GTG CGC GGA GTT GAT ATG TTA GCA GAT ACC GTC AAA GTA 98
Ala Ala Met Val Arg Gly Val Asp Met Leu Ala Asp Thr Val Lys Val
15 20 25

ACG CTT GGT CCT AAA GGG CGC AAT GTT GTT CTT GAA AAA GCT TTT GGT 146
Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Ala Phe Gly
30 35 40

TCT CCC TTA ATT ACT AAT GAC GGG GTA ACC ATT GCT AAA GAG ATC GAA 194
Ser Pro Leu Ile Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu
45 50 55 60

TTA GAA GAT CAT TTT GAA AAC ATG GGA GCA AAA TTG GTG TCT GAA GTG 242
Leu Glu Asp His Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val
65 70 75

GCT TCT AAA ACC AAT GAT ATT GCT GGT GAT GGG ACG ACT ACT GCA ACA 290
Ala Ser Lys Thr Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr
80 85 90

GTT TTG ACA CAA GCC ATT GTT CAT GAA GGA CTA AAA AAT GTG ACA GCA 338
Val Leu Thr Gln Ala Ile Val His Glu Gly Leu Lys Asn Val Thr Ala
95 100 105

GGT GCT AAT CCA ATT GGT ATC CGT CGA GGC ATT GAA ACA GCA ACA GCA 386
Gly Ala Asn Pro Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Thr Ala
110 115 120

ACA GCT GTT GAA GCC TTG AAA GCC ATT GCT CAA CCT GTA TCT GGC AAG 434
Thr Ala Val Glu Ala Leu Lys Ala Ile Ala Gln Pro Val Ser Gly Lys
125 130 135 140

GAA GCT ATT GCT CAG GTC GCT GCA GTA TCA TCA CGC TCT GAA AAA GTT 482
Glu Ala Ile Ala Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val
145 150 155

GGA GAG TAT ATC TCA GAA GCT ATG GAG CGT GTG GGC AAC GAT GGT GTG 530
Gly Glu Tyr Ile Ser Glu Ala Met Glu Arg Val Gly Asn Asp Gly Val
160 165 170

ATT ACC ATC GAA GAA TCT CGA GGT ATG GAA ACA GAA CTT GAA GTG GTT 578
Ile Thr Ile Glu Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val
175 180 185

GAA GGC ATG CAA TTT GAC CGT GGT TAC CTG TCT CAA TAC ATG GTC ACA 626
Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr
190 195 200

GAC AAT GAA AAA ATG GTT GCA GAC CTT GAA AAC CCA TTT ATC TTA ATC 674

Asp Asn Glu Lys Met Val Ala Asp Leu Glu Asn Pro Phe Ile Leu Ile
 205 210 215 220

ACG GAT AAA AAA GTG TCA AAC ATC CAA GAC ATT TTG CCA CTA CTT GAG 722
 Thr Asp Lys Lys Val Ser Asn Ile Gln Asp Ile Leu Pro Leu Leu Glu
 225 230 235

GAA GTT CTT AAA ACC AAC CGT CCA TTA CTC ATT ATT GCA GAT GAT GTG 770
 Glu Val Leu Lys Thr Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val
 240 245 250

GAT GGT GAA GCA CTT CCA ACC CTT GTC TTG AAC AAG ATT CGT GGT ACT 818
 Asp Gly Glu Ala Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr
 255 260 265

TTC AAT GTG GTT GCT GTC AAA GCG CCA GGA TTT GGT GAT CGT CGT AAA 866
 Phe Asn Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys
 270 275 280

GCT ATG CTT GAA GAC ATT GCT ATC TTG ACA GGT GGT ACA GTG ATT ACA 914
 Ala Met Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Thr
 285 290 295 300

GAG GAT CTA GGA CTT GAA TTA AAA GAT GCT ACA ATG ACA GCC CTT GGA 962
 Glu Asp Leu Gly Leu Glu Leu Lys Asp Ala Thr Met Thr Ala Leu Gly
 305 310 315

CAG GCT GCT AAG ATT ACA GTT GAT AAA GAT AGC ACA GTA ATT GTT GAA 1010
 Gln Ala Ala Lys Ile Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu
 320 325 330

GGT TCA GGA AGT TCA GAA GCT ATT GCT AAC CGT ATT GCA CTG ATT AAA 1058
 Gly Ser Gly Ser Ser Glu Ala Ile Ala Asn Arg Ile Ala Leu Ile Lys
 335 340 345

TCG CAA TTA GAA ACA ACA ACT TCT GAC TTT GAC CGT GAA AAA CTA CAA 1106
 Ser Gln Leu Glu Thr Thr Thr Ser Asp Phe Asp Arg Glu Lys Leu Gln
 350 355 360

GAA CGT TTG GCG AAA TTA GCT GGT GGT GTA GCT GTT ATC AAA GTA GGA 1154
 Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly
 365 370 375 380

GCT CCA ACA GAG ACA GCT TTA AAA GAA ATG AAA CTT CGC ATT GAG GAT 1202
 Ala Pro Thr Glu Thr Ala Leu Lys Glu Met Lys Leu Arg Ile Glu Asp
 385 390 395

GCT CTA AAT GCT ACA CGT GCA GCC GTT GAA GAA GGT ATC GTT GCT GGT 1250
 Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly
 400 405 410

GGT GGA ACA GCA CTT ATT ACG GTT ATT GAA AAA GTA GCA GCT CTT GAG 1298
 Gly Gly Thr Ala Leu Ile Thr Val Ile Glu Lys Val Ala Ala Leu Glu
 415 420 425

CTT GAG GGC GAT GAT GCT ACT GGA CGT AAC ATT GTG CTT CGT GCT CTA 1346
 Leu Glu Gly Asp Asp Ala Thr Gly Arg Asn Ile Val Leu Arg Ala Leu
 430 435 440

GAA GAG CCT GTA CGT CAA ATT GCT TTA AAT GCT GGG TAC GAA GGC TCC Glu Glu Pro Val Arg Gln Ile Ala Leu Asn Ala Gly Tyr Glu Gly Ser 445 450 455 460	1394
GTA GTT ATT GAC AAG TTG AAA AAC AGC CCT GCA GGA ACA GGA TTT AAT Val Val Ile Asp Lys Leu Lys Asn Ser Pro Ala Gly Thr Gly Phe Asn 465 470 475	1442
GCT GCA ACA GGT GAG TGG GTT GAT ATG ATT AAA ACA GGA ATC ATT GAC Ala Ala Thr Gly Glu Trp Val Asp Met Ile Lys Thr Gly Ile Ile Asp 480 485 490	1490
CCT GTC AAA GTA ACA CGA TCA GCG CTT CAA AAT GCA GCT TCT GTA GCT Pro Val Lys Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala 495 500 505	1538
AGT CTT ATT TTG ACA ACA GAA GCA GTT GTT GCT AAT AAA CCT GAA CCA Ser Leu Ile Leu Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro 510 515 520	1586
GCT ACG CCA GCG CCA GCA ATG CCA GCA GGT ATG GAT CCA GGA ATG ATG Ala Thr Pro Ala Pro Ala Met Pro Ala Gly Met Asp Pro Gly Met Met 525 530 535 540	1634
GGT GGG ATG GGC GGA TAAGCCGAAT TC Gly Gly Met Gly Gly 545	1661

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Lys Glu Ile Lys Phe Ser Ala Asp Ala Arg Ala Ala Met Val 1 5 10 15
Arg Gly Val Asp Met Leu Ala Asp Thr Val Lys Val Thr Leu Gly Pro 20 25 30
Lys Gly Arg Asn Val Val Leu Glu Lys Ala Phe Gly Ser Pro Leu Ile 35 40 45
Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His 50 55 60
Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val Ala Ser Lys Thr 65 70 75 80
Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Gln 85 90 95

Ala Ile Val His Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro
 100 105 110
 Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Thr Ala Thr Ala Val Glu
 115 120 125
 Ala Leu Lys Ala Ile Ala Gln Pro Val Ser Gly Lys Glu Ala Ile Ala
 130 135 140
 Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val Gly Glu Tyr Ile
 145 150 155 160
 Ser Glu Ala Met Glu Arg Val Gly Asn Asp Gly Val Ile Thr Ile Glu
 165 170 175
 Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val Glu Gly Met Gln
 180 185 190
 Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr Asp Asn Glu Lys
 195 200 205
 Met Val Ala Asp Leu Glu Asn Pro Phe Ile Leu Ile Thr Asp Lys Lys
 210 215 220
 Val Ser Asn Ile Gln Asp Ile Leu Pro Leu Leu Glu Glu Val Leu Lys
 225 230 235 240
 Thr Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val Asp Gly Glu Ala
 245 250 255
 Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr Phe Asn Val Val
 260 265 270
 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Glu
 275 280 285
 Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Thr Glu Asp Leu Gly
 290 295 300
 Leu Glu Leu Lys Asp Ala Thr Met Thr Ala Leu Gly Gln Ala Ala Lys
 305 310 315 320
 Ile Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu Gly Ser Gly Ser
 325 330 335
 Ser Glu Ala Ile Ala Asn Arg Ile Ala Leu Ile Lys Ser Gln Leu Glu
 340 345 350
 Thr Thr Thr Ser Asp Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Pro Thr Glu
 370 375 380
 Thr Ala Leu Lys Glu Met Lys Leu Arg Ile Glu Asp Ala Leu Asn Ala
 385 390 395 400

Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Thr Ala
 405 410 415
 Leu Ile Thr Val Ile Glu Lys Val Ala Ala Leu Glu Leu Glu Gly Asp
 420 425 430
 Asp Ala Thr Gly Arg Asn Ile Val Leu Arg Ala Leu Glu Glu Pro Val
 435 440 445
 Arg Gln Ile Ala Leu Asn Ala Gly Tyr Glu Gly Ser Val Val Ile Asp
 450 455 460
 Lys Leu Lys Asn Ser Pro Ala Gly Thr Gly Phe Asn Ala Ala Thr Gly
 465 470 475 480
 Glu Trp Val Asp Met Ile Lys Thr Gly Ile Ile Asp Pro Val Lys Val
 485 490 495
 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Ile Leu
 500 505 510
 Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Ala Thr Pro Ala
 515 520 525
 Pro Ala Met Pro Ala Gly Met Asp Pro Gly Met Met Gly Gly Met Gly
 530 535 540
 Gly
 545

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Lys Glu Ile Lys Phe Ser Glu Glu Ala Arg Arg Ala Met Leu
 1 5 10 15
 Arg Gly Val Asp Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro
 20 25 30
 Lys Gly Arg Asn Val Val Leu Glu Lys Lys Phe Gly Ser Pro Leu Ile
 35 40 45
 Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp Ala
 50 55 60
 Phe Glu Asn Met Gly Ala Lys Leu Val Ala Glu Val Ala Ser Lys Thr
 65 70 75 80

Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
 85 90 95
 Ala Met Ile Arg Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro
 100 105 110
 Val Gly Val Arg Lys Gly Met Glu Gln Ala Val Ala Val Ala Ile Glu
 115 120 125
 Asn Leu Lys Glu Ile Ser Lys Pro Ile Glu Gly Lys Glu Ser Ile Ala
 130 135 140
 Gln Val Ala Ala Ile Ser Ala Ala Asp Glu Glu Val Gly Ser Leu Ile
 145 150 155 160
 Ala Glu Ala Met Glu Arg Val Gly Asn Asp Gly Val Ile Thr Ile Glu
 165 170 175
 Glu Ser Lys Gly Phe Thr Thr Glu Leu Glu Val Val Glu Gly Met Gln
 180 185 190
 Phe Asp Arg Gly Tyr Ala Ser Pro Tyr Met Val Thr Asp Ser Asp Lys
 195 200 205
 Met Glu Ala Val Leu Asp Asn Pro Tyr Ile Leu Ile Thr Asp Lys Lys
 210 215 220
 Ile Thr Asn Ile Gln Glu Ile Leu Pro Val Leu Glu Gln Val Val Gln
 225 230 235 240
 Gln Gly Lys Pro Leu Leu Leu Ile Ala Glu Asp Val Glu Gly Glu Ala
 245 250 255
 Leu Ala Thr Leu Val Val Asn Lys Leu Arg Gly Thr Phe Asn Ala Val
 260 265 270
 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Glu
 275 280 285
 Asp Ile Ala Val Leu Thr Gly Gly Glu Val Ile Thr Glu Asp Leu Gly
 290 295 300
 Leu Asp Leu Lys Ser Thr Gln Ile Ala Gln Leu Gly Arg Ala Ser Lys
 305 310 315 320
 Val Val Val Thr Lys Glu Asn Thr Thr Ile Val Glu Gly Ala Gly Glu
 325 330 335
 Thr Asp Lys Ile Ser Ala Arg Val Thr Gln Ile Arg Ala Gln Val Glu
 340 345 350
 Glu Thr Thr Ser Glu Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu
 370 375 380

Thr	Glu	Leu	Lys	Glu	Arg	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Leu	Asn	Ser	385	390	395	400
Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ser	Gly	Gly	Gly	Thr	Ala	405	410	415	
Leu	Val	Asn	Val	Tyr	Asn	Lys	Val	Ala	Ala	Val	Glu	Ala	Glu	Gly	Asp	420	425	430	
Ala	Gln	Thr	Gly	Ile	Asn	Ile	Val	Leu	Arg	Ala	Leu	Glu	Glu	Pro	Ile	435	440	445	
Arg	Gln	Ile	Ala	His	Asn	Ala	Gly	Leu	Glu	Gly	Ser	Val	Ile	Val	Glu	450	455	460	
Arg	Leu	Lys	Asn	Glu	Glu	Ile	Gly	Val	Gly	Phe	Asn	Ala	Ala	Thr	Gly	465	470	475	480
Glu	Trp	Val	Asn	Met	Ile	Glu	Lys	Gly	Ile	Val	Asp	Pro	Thr	Lys	Val	485	490	495	
Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Val	Ala	Ala	Met	Phe	Leu	500	505	510	
Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Glu	Asn	Gly	Gly	Gly	515	520	525	
Ala	Gly	Met	Pro	Asp	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Met	530	535	540	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Lys	Thr	Leu	Leu	Phe	Gly	Glu	Glu	Ala	Arg	Arg	Ser	Met	Gln	1	5	10	15
Ala	Gly	Val	Asp	Lys	Leu	Ala	Asn	Thr	Val	Lys	Val	Thr	Leu	Gly	Pro	20	25	30	
Lys	Gly	Arg	Asn	Val	Ile	Leu	Asp	Lys	Lys	Phe	Gly	Ser	Pro	Leu	Ile	35	40	45	
Thr	Asn	Asp	Gly	Val	Thr	Ile	Ala	Arg	Glu	Ile	Glu	Leu	Glu	Asp	Ala	50	55	60	
Tyr	Glu	Asn	Met	Gly	Ala	Gln	Leu	Val	Lys	Glu	Val	Ala	Thr	Lys	Thr				

65 70 75 80
 Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
 85 90 95
 Ala Ile Ile Arg Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro
 100 105 110
 Ile Leu Ile Arg Asn Gly Ile Lys Thr Ala Val Glu Lys Ala Val Glu
 115 120 125
 Glu Ile Gln Lys Ile Ser Lys Pro Val Asn Gly Lys Glu Asp Ile Ala
 130 135 140
 Arg Val Ala Ala Ile Ser Ala Ala Asp Glu Lys Ile Gly Lys Leu Ile
 145 150 155 160
 Ala Asp Ala Met Glu Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu
 165 170 175
 Glu Ser Lys Ser Met Gly Thr Glu Leu Asp Val Val Glu Gly Met Gln
 180 185 190
 Phe Asp Arg Gly Tyr Val Ser Ala Tyr Met Val Thr Asp Thr Glu Lys
 195 200 205
 Met Glu Ala Val Leu Asp Asn Pro Leu Val Leu Ile Thr Asp Lys Lys
 210 215 220
 Ile Ser Asn Ile Gln Asp Leu Leu Pro Leu Leu Glu Gln Ile Val Gln
 225 230 235 240
 Ala Gly Lys Lys Leu Leu Ile Ile Ala Asp Asp Ile Glu Gly Glu Ala
 245 250 255
 Met Thr Thr Leu Val Val Asn Lys Leu Arg Gly Thr Phe Thr Cys Val
 260 265 270
 Gly Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu Gln
 275 280 285
 Asp Ile Ala Thr Leu Thr Gly Gly Val Val Ile Ser Asp Glu Val Gly
 290 295 300
 Gly Asp Leu Lys Glu Ala Thr Leu Asp Met Leu Gly Glu Ala Glu Ser
 305 310 315 320
 Val Lys Val Thr Lys Glu Ser Thr Thr Ile Val Asn Gly Arg Gly Asn
 325 330 335
 Ser Glu Glu Ile Lys Asn Arg Ile Asn Gln Ile Lys Leu Gln Leu Glu
 340 345 350
 Ala Thr Thr Ser Glu Phe Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Val Lys Val Gly Ala Ala Thr Glu
 370 375 380

Thr Glu Leu Lys Glu Ser Lys Leu Arg Ile Glu Asp Ala Leu Ala Ala
 385 390 395 400
 Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Thr Ala
 405 410 415
 Tyr Val Asn Val Ile Asn Glu Val Ala Lys Leu Thr Ser Asp Ile Gln
 420 425 430
 Asp Glu Gln Val Gly Ile Asn Ile Ile Val Arg Ser Leu Glu Glu Pro
 435 440 445
 Met Arg Gln Ile Ala His Asn Ala Gly Leu Glu Gly Ser Val Ile Ile
 450 455 460
 Glu Lys Val Lys Asn Ser Asp Ala Gly Val Gly Phe Asp Ala Leu Arg
 465 470 475 480
 Gly Glu Tyr Lys Asp Met Ile Lys Ala Gly Ile Val Asp Pro Thr Lys
 485 490 495
 Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Thr Phe
 500 505 510
 Leu Thr Thr Glu Ala Ala Val Ala Asp Ile Pro Glu Lys Glu Met Pro
 515 520 525
 Gln Gly Ala Gly Met Gly Met Asp Gly Met Tyr
 530 535

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Asn Met Val Val Thr Gly Glu Gln Leu Asp Lys Ser Ile Arg
 1 5 10 15
 Glu Val Val Arg Ile Leu Glu Asp Ala Val Gly Cys Thr Ala Gly Pro
 20 25 30
 Lys Gly Leu Thr Val Ala Ile Ser Lys Pro Tyr Gly Ala Pro Glu Val
 35 40 45
 Thr Lys Asp Gly Tyr Lys Val Met Lys Ser Ile Lys Pro Glu Asp Pro
 50 55 60
 Leu Ala Leu Ala Ile Ala Asn Ile Ile Ala Gln Ser Ala Ser Gln Cys

65					70					75					80				
Asn	Asp	Lys	Val	Gly	Asp	Gly	Thr	Thr	Thr	Cys	Ser	Ile	Leu	Thr	Ala				
85					90					95									
Lys	Val	Ile	Glu	Glu	Val	Ser	Lys	Val	Lys	Ala	Ala	Gly	Ala	Asp	Ile				
100					105					110									
Ile	Cys	Val	Arg	Glu	Gly	Val	Leu	Lys	Ala	Lys	Glu	Ala	Val	Leu	Glu				
115					120					125									
Ala	Leu	Lys	Cys	Met	Lys	Arg	Glu	Val	Leu	Ser	Glu	Glu	Glu	Ile	Ala				
130					135					140									
Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Lys	Asn	Ile	Gly	Thr	Lys				
145					150					155									
Ile	Ala	Gln	Cys	Val	Lys	Glu	Val	Gly	Lys	Asp	Gly	Val	Ile	Thr	Val				
165					170					175									
Glu	Glu	Ser	Lys	Gly	Phe	Lys	Glu	Leu	Asp	Val	Glu	Lys	Thr	Asp	Gly				
180					185					190									
Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Val	Thr	Asn	Ser				
195					200					205									
Glu	Lys	Met	Leu	Val	Glu	Phe	Glu	Asn	Pro	Tyr	Ile	Leu	Leu	Thr	Glu				
210					215					220									
Lys	Lys	Leu	Asn	Ile	Ile	Gln	Pro	Leu	Leu	Pro	Ile	Leu	Glu	Asn	Ile				
225					230					235									
Ala	Arg	Ser	Gly	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly				
245					250					255									
Glu	Ala	Leu	Ser	Thr	Leu	Val	Leu	Asn	Lys	Leu	Arg	Gly	Gly	Leu	His				
260					265					270									
Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Asp	Met				
275					280					285									
Leu	Gly	Asp	Ile	Ala	Ile	Leu	Thr	Gly	Ala	Lys	His	Val	Ile	Asn	Asp				
290					295					300									
Glu	Leu	Ala	Ile	Lys	Met	Glu	Asp	Leu	Thr	Leu	Cys	Asp	Leu	Gly	Thr				
305					310					315									
Ala	Lys	Asn	Ile	Arg	Ile	Thr	Lys	Asp	Thr	Thr	Thr	Thr	Ile	Ile	Gly				
325					330					335									
Val	Asp	Asn	Ser	Cys	Ala	His	Val	Gln	Ser	Arg	Ile	Cys	Gln	Ile	Arg				
340					345					350									
Met	Gln	Ile	Asp	Asn	Ser	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	Gln				
355					360					365									
Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	Leu	Lys	Val	Gly				
370					375					380									

Gly Ser Ser Glu Val Glu Val Lys Glu Arg Lys Asp Arg Val Glu Asp
 385 390 395 400
 Ala Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Pro Gly
 405 410 415
 Gly Gly Ala Ala Leu Leu Tyr Thr Leu Ser Ala Leu Asp Asn Leu Lys
 420 425 430
 Ser Lys Asn Asp Asp Glu Gln Leu Gly Ile Asn Ile Val Lys Arg Ala
 435 440 445
 Leu Gln Ala Pro Ile Lys Arg Ile Ile Lys Asn Ala Gly Ser Glu Asn
 450 455 460
 Ala Pro Cys Val Ile Ala His Leu Leu Lys Gln Asn Asp Lys Glu Leu
 465 470 475 480
 Ile Phe Asn Val Asp Val Thr Asn Phe Ala Asn Ala Phe Thr Ser Gly
 485 490 495
 Val Ile Asp Pro Leu Lys Val Val Arg Ile Ala Phe Asp Phe Ala Val
 500 505 510
 Ser Leu Ala Ala Val Phe Met Thr Leu Asn Ala Ile Val Val Asp Ile
 515 520 525
 Pro Ser Lys Asp Asp Asn Ser Ala Ala Gly Gly Ala Gly Met Gly Gly
 530 535 540
 Met Gly Gly Met Gly Gly Phe
 545 550

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met
 1 5 10 15
 Leu Asn Gly Val Asn Ile Leu Ala Asp Ala Val Lys Val Thr Leu Gly
 20 25 30
 Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
 35 40 45
 Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp

50	55	60
Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys		
65	70	75 80
Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala		
	85	90 95
Gln Ala Ile Val Asn Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn		
	100	105 110
Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Asn Ser Val Val		
	115	120 125
Ala Glu Leu Lys Asn Leu Ser Lys Pro Cys Glu Thr Ser Lys Glu Ile		
	130	135 140
Glu Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Ser Ile Val Gly Gln		
	145	150 155 160
Leu Ile Ala Gln Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr		
	165	170 175
Val Glu Asp Gly Thr Gly Leu Glu Asp Glu Leu Asp Val Val Glu Gly		
	180	185 190
Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro		
	195	200 205
Glu Thr Ala Gly Thr Val Glu Leu Asp Asn Pro Phe Ile Leu Leu Val		
	210	215 220
Asp Lys Lys Ile Ser Asn Ile Arg Glu Leu Leu Pro Val Leu Glu Ala		
	225	230 235 240
Val Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu		
	245	250 255
Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val		
	260	265 270
Lys Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala		
	275	280 285
Met Leu Gln Asp Ile Ala Ile Leu Thr Ala Gly Thr Val Ile Ser Glu		
	290	295 300
Glu Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Glu Leu Gly Gln		
	305	310 315 320
Ala Lys Arg Val Val Ile Thr Lys Asp Asn Thr Thr Ile Ile Asp Gly		
	325	330 335
Ile Gly Asp Glu Ala Gln Ile Lys Ala Arg Val Val Gln Ile Arg Gln		
	340	345 350
Gln Ile Glu Asp Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu		
	355	360 365

Arg Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala
 370 375 380
 Ala Thr Glu Val Ala Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala
 385 390 395 400
 Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly
 405 410 415
 Gly Val Ala Leu Val Arg Ala Ala Asn Lys Val Ser Ala Thr Leu Thr
 420 425 430
 Gly Asp Asn Glu Glu Gln Asn Val Gly Ile Lys Leu Ala Leu Arg Ala
 435 440 445
 Met Glu Ala Pro Leu Arg Gln Ile Val Glu Asn Ser Gly Glu Asp Ala
 450 455 460
 Ser Val Val Ala Arg Asp Val Lys Asp Gly Ser Gly Asn Phe Gly Tyr
 465 470 475 480
 Asn Ala Thr Thr Glu Glu Tyr Gly Asp Met Leu Glu Met Gly Ile Leu
 485 490 495
 Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Phe Ala Ala Ser Ile
 500 505 510
 Ala Gly Leu Met Ile Thr Thr Glu Cys Met Ile Thr Asp Leu Pro Lys
 515 520 525
 Glu Asp Lys Leu Asp Ala Gln Ala Ala Met Gly Gly Met Gly Gly Met
 530 535 540
 Gly Gly Met Met
 545

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ala Lys Glu Leu Arg Phe Gly Asp Asp Ala Arg Leu Gln Met Leu
 1 5 10 15
 Ala Gly Val Asn Ala Leu Ala Asp Ala Val Gln Val Thr Met Gly Pro
 20 25 30
 Arg Gly Arg Asn Val Val Leu Glu Lys Ser Tyr Gly Ala Pro Thr Val

35	40	45
Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Phe Glu His Arg		
50	55	60
Phe Met Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys Thr		
65	70	75 80
Ser Asp Thr Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Arg		
	85	90 95
Ser Ile Leu Val Glu Gly His Lys Ala Val Ala Ala Gly Met Asn Pro		
	100	105 110
Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Leu Ala Val Thr Lys		
	115	120 125
Lys Leu Gln Ala Met Ser Lys Pro Cys Lys Asp Ser Lys Ala Ile Ala		
	130	135 140
Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Ala Ile Gly Ala Ile		
	145	150 155 160
Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr Val		
	165	170 175
Glu Asp Gly Asn Gly Leu Glu Asn Glu Leu Ser Val Val Glu Gly Met		
	180	185 190
Gln Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Asn Gln Gln		
	195	200 205
Asn Met Ser Cys Glu Leu Glu His Pro Phe Ile Leu Leu Val Asp Lys		
	210	215 220
Lys Val Ser Ser Ile Arg Glu Met Leu Ser Val Leu Glu Gly Val Ala		
	225	230 235 240
Lys Ser Gly Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu		
	245	250 255
Ala Leu Ala Thr Leu Val Val Asn Asn Met Arg Gly Ile Val Lys Val		
	260	265 270
Cys Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu		
	275	280 285
Gln Asp Ile Ala Ile Leu Thr Lys Gly Gln Val Ile Ser Glu Glu Ile		
	290	295 300
Gly Lys Ser Leu Glu Gly Ala Thr Leu Glu Asp Leu Gly Ser Ala Lys		
	305	310 315 320
Arg Ile Val Val Thr Lys Glu Asn Thr Thr Ile Ile Asp Gly Glu Gly		
	325	330 335
Lys Ala Thr Glu Ile Asn Ala Arg Ile Thr Gln Ile Arg Ala Gln Met		
	340	345 350

Glu Glu Thr Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Val
 355 360 365
 Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr
 370 375 380
 Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu His
 385 390 395 400
 Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val
 405 410 415
 Ala Leu Ile Arg Ala Gln Lys Ala Leu Asp Ser Leu Lys Gly Asp Asn
 420 425 430
 Asp Asp Gln Asn Met Gly Ile Asn Ile Leu Arg Arg Ala Ile Glu Ser
 435 440 445
 Pro Met Arg Gln Ile Val Thr Asn Ala Gly Tyr Glu Ala Ser Val Val
 450 455 460
 Val Asn Lys Val Ala Glu His Lys Asp Asn Tyr Gly Phe Asn Ala Ala
 465 470 475 480
 Thr Gly Glu Tyr Gly Asp Met Val Glu Met Gly Ile Leu Asp Pro Thr
 485 490 495
 Lys Val Thr Arg Met Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu
 500 505 510
 Met Leu Thr Thr Glu Cys Met Val Ala Asp Leu Pro Lys Lys Glu Glu
 515 520 525
 Gly Val Gly Ala Gly Asp Met Gly Gly Met Gly Gly Met Gly Gly Met
 530 535 540
 Gly Gly Met Met Glx
 545

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu
 1 5 10 15
 Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro

20 25 30
 Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
 35 40 45
 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
 50 55 60
 Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
 65 70 75 80
 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
 85 90 95
 Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 100 105 110
 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu
 115 120 125
 Thr Leu Leu Lys Ser Ala Lys Glu Val Glu Thr Lys Asp Gln Ile Ala
 130 135 140
 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile
 145 150 155 160
 Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu
 165 170 175
 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
 180 185 190
 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg
 195 200 205
 Gln Glu Ala Val Leu Glu Asp Pro Phe Ile Leu Leu Val Ser Ser Lys
 210 215 220
 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln
 225 230 235 240
 Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala
 245 250 255
 Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val
 260 265 270
 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln
 275 280 285
 Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Val Gly
 290 295 300
 Leu Ser Leu Glu Ser Ala Asp Ile Ser Leu Leu Gly Lys Ala Arg Lys
 305 310 315 320
 Val Val Val Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp
 325 330 335

Ser Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Thr Glu Ile Glu
 340 345 350
 Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu
 370 375 380
 Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn
 385 390 395 400
 Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Ala
 405 410 415
 Leu Leu His Ala Ile Pro Ala Leu Asp Glu Leu Lys Pro Glu Gly Glu
 420 425 430
 Glu Ala Thr Gly Ala Asn Ile Val Arg Val Ala Leu Glu Arg Pro Leu
 435 440 445
 Lys Gln Ile Ala Phe Asn Gly Gly Leu Glu Pro Gly Val Val Ala Glu
 450 455 460
 Lys Val Arg Asn Ser Pro Ala Gly Thr Gly Leu Asn Ala Ala Thr Gly
 465 470 475 480
 Glu Tyr Glu Asp Leu Leu Lys Ala Gly Ile Ala Asp Pro Val Lys Val
 485 490 495
 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu
 500 505 510
 Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Ala Ala Ala Pro
 515 520 525
 Ala Gly Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe
 530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu
 1 5 10 15
 Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro

20										25										30										
Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala	Pro	Thr	Ile															
			35				40					45																		
Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu	Leu	Glu	Asp	Pro															
		50				55					60																			
Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu	Val	Ala	Lys	Lys	Thr															
	65				70					75					80															
Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln															
				85					90					95																
Ala	Leu	Val	Arg	Glu	Gly	Leu	Arg	Asn	Val	Ala	Ala	Gly	Ala	Asn	Pro															
			100					105					110																	
Leu	Gly	Leu	Lys	Arg	Gly	Ile	Glu	Lys	Ala	Val	Glu	Lys	Val	Thr	Glu															
		115					120					125																		
Thr	Leu	Leu	Lys	Gly	Ala	Lys	Glu	Val	Glu	Thr	Lys	Glu	Gln	Ile	Ala															
		130				135					140																			
Ala	Thr	Ala	Ala	Ile	Ser	Ala	Gly	Asp	Gln	Ser	Ile	Gly	Asp	Leu	Ile															
		145				150				155					160															
Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Asn	Glu	Gly	Val	Ile	Thr	Val	Glu															
				165					170					175																
Glu	Ser	Asn	Thr	Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr	Glu	Gly	Met	Arg															
			180					185					190																	
Phe	Asp	Lys	Gly	Tyr	Ile	Ser	Gly	Tyr	Phe	Val	Thr	Asp	Pro	Glu	Arg															
		195					200					205																		
Gln	Glu	Ala	Val	Leu	Glu	Asp	Pro	Tyr	Ile	Leu	Leu	Val	Ser	Ser	Lys															
		210				215					220																			
Val	Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ile	Gly															
		225			230					235					240															
Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala															
				245					250					255																
Leu	Ser	Thr	Leu	Val	Val	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Lys	Ser	Val															
			260					265					270																	
Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln															
		275					280					285																		
Asp	Met	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser	Glu	Glu	Val	Gly															
		290				295					300																			
Leu	Thr	Leu	Glu	Asn	Ala	Asp	Leu	Ser	Leu	Leu	Gly	Lys	Ala	Arg	Lys															
		305			310					315					320															
Val	Val	Val	Thr	Lys	Asp	Glu	Thr	Thr	Ile	Val	Glu	Gly	Ala	Gly	Asp															
				325					330					335																

61

Thr Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Gln Glu Ile Glu
 340 345 350
 Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu
 370 375 380
 Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn
 385 390 395 400
 Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr
 405 410 415
 Leu Leu Gln Ala Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp
 420 425 430
 Glu Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu
 435 440 445
 Lys Gln Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu
 450 455 460
 Lys Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly
 465 470 475 480
 Val Tyr Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys Val
 485 490 495
 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu
 500 505 510
 Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu Lys Ala Ser
 515 520 525
 Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe
 530 535 540

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ser Lys Leu Ile Glu Tyr Asp Glu Thr Ala Arg His Ala Met Glu
 1 5 10 15
 Val Gly Met Asn Lys Leu Ala Asp Thr Val Arg Val Thr Leu Gly Pro

20					25					30					
Arg	Gly	Arg	His	Val	Val	Leu	Ala	Lys	Ala	Phe	Gly	Gly	Pro	Thr	Ile
	35						40					45			
Thr	Asn	Asp	Gly	Val	Thr	Val	Ala	Arg	Glu	Ile	Asp	Leu	Glu	Asp	Pro
	50					55					60				
Phe	Glu	Asn	Leu	Gly	Ala	Gln	Leu	Val	Lys	Ser	Val	Ala	Thr	Lys	Thr
65					70					75					80
Asn	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln
				85					90					95	
Ala	Leu	Val	Lys	Gly	Gly	Leu	Arg	Met	Val	Ala	Ala	Gly	Ala	Asn	Pro
			100					105					110		
Val	Ala	Leu	Gly	Ala	Gly	Ile	Ser	Lys	Ala	Ala	Asp	Ala	Val	Ser	Glu
		115					120					125			
Ala	Leu	Leu	Ala	Val	Ala	Thr	Pro	Val	Ala	Gly	Lys	Asp	Ala	Ile	Thr
	130					135						140			
Gln	Val	Ala	Thr	Val	Ser	Ser	Arg	Asp	Glu	Gln	Ile	Gly	Ala	Leu	Val
145						150					155				160
Gly	Glu	Gly	Met	Asn	Lys	Val	Gly	Thr	Asp	Gly	Val	Val	Ser	Val	Glu
			165						170					175	
Glu	Ser	Ser	Thr	Leu	Asp	Thr	Glu	Leu	Glu	Phe	Thr	Glu	Gly	Val	Gly
			180					185					190		
Phe	Asp	Lys	Gly	Phe	Leu	Ser	Ala	Tyr	Phe	Val	Thr	Asp	Phe	Asp	Ser
		195					200					205			
Gln	Gln	Ala	Val	Leu	Asp	Asp	Pro	Leu	Val	Leu	Leu	His	Gln	Glu	Lys
	210					215					220				
Ile	Ser	Ser	Leu	Pro	Glu	Leu	Leu	Pro	Met	Leu	Glu	Lys	Val	Thr	Glu
225						230					235				240
Ser	Gly	Lys	Pro	Leu	Leu	Ile	Val	Ala	Glu	Asp	Leu	Glu	Gly	Glu	Ala
				245					250					255	
Leu	Ala	Thr	Leu	Val	Val	Asn	Ser	Ile	Arg	Lys	Thr	Leu	Lys	Ala	Val
			260					265					270		
Ala	Val	Lys	Ser	Pro	Phe	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Phe	Leu	Glu
		275					280					285			
Asp	Leu	Ala	Ile	Val	Thr	Gly	Gly	Gln	Val	Val	Asn	Pro	Glu	Thr	Gly
	290					295					300				
Leu	Val	Leu	Arg	Glu	Val	Gly	Thr	Asp	Val	Leu	Gly	Ser	Ala	Arg	Arg
305						310					315				320
Val	Val	Val	Ser	Lys	Asp	Asp	Thr	Ile	Ile	Val	Asp	Gly	Gly	Gly	Ser
				325					330					335	

C1

Asn Asp Ala Val Ala Lys Arg Val Asn Gln Leu Arg Ala Glu Ile Glu
 340 345 350
 Val Ser Asp Ser Glu Trp Asp Arg Glu Lys Leu Gln Glu Arg Val Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Val Thr Glu
 370 375 380
 Thr Ala Leu Lys Lys Arg Lys Glu Ser Val Glu Asp Ala Val Ala Ala
 385 390 395 400
 Ala Lys Ala Ser Ile Glu Glu Gly Ile Ile Ala Gly Gly Gly Ser Ala
 405 410 415
 Leu Val Gln Cys Gly Ala Ala Leu Lys Gln Leu Arg Thr Ser Leu Thr
 420 425 430
 Gly Asp Glu Ala Leu Gly Ile Asp Val Phe Phe Glu Ala Leu Lys Ala
 435 440 445
 Pro Leu Tyr Trp Ile Ala Thr Asn Ala Gly Leu Asp Gly Ala Val Val
 450 455 460
 Val Asp Lys Val Ser Gly Leu Pro Ala Gly His Gly Leu Asn Ala Ser
 465 470 475 480
 Thr Leu Gly Tyr Gly Asp Leu Val Ala Asp Gly Val Val Asp Pro Val
 485 490 495
 Lys Val Thr Arg Ser Ala Val Leu Asn Ala Ala Ser Val Ala Arg Met
 500 505 510
 Met Leu Thr Thr Glu Thr Ala Val Val Asp Lys Pro Ala Lys Thr Glu
 515 520 525
 Glu His Asp His His Gly His Ala His
 530 535

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu
 1 5 10 15
 Arg Gly Leu Asn Ser Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro

20 25 30
 Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
 35 40 45
 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
 50 55 60
 Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
 65 70 75 80
 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
 85 90 95
 Ala Leu Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 100 105 110
 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Lys Val Thr Glu
 115 120 125
 Thr Leu Leu Lys Asp Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala
 130 135 140
 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile
 145 150 155 160
 Ala Glu Ala Met Asp Lys Val Gly Met Glu Gly Val Ile Thr Val Glu
 165 170 175
 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
 180 185 190
 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg
 195 200 205
 Gln Glu Ala Val Leu Glu Glu Pro Tyr Ile Leu Leu Val Ser Ser Lys
 210 215 220
 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln
 225 230 235 240
 Ala Gly Lys Ser Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala
 245 250 255
 Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val
 260 265 270
 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln
 275 280 285
 Asp Met Ala Ile Leu Thr Gly Ala Gln Val Ile Ser Glu Glu Val Gly
 290 295 300
 Leu Thr Leu Glu Asn Thr Asp Leu Ser Leu Leu Gly Lys Ala Arg Lys
 305 310 315 320
 Val Val Met Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp
 325 330 335

Thr Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Thr Glu Ile Glu
 340 345 350
 Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu
 370 375 380
 Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn
 385 390 395 400
 Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr
 405 410 415
 Leu Leu Gln Ala Ala Pro Ala Leu Asp Lys Leu Lys Leu Thr Gly Asp
 420 425 430
 Glu Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu
 435 440 445
 Lys Gln Ile Ala Phe Asn Ser Gly Met Glu Pro Gly Val Val Ala Glu
 450 455 460
 Lys Val Arg Asn Leu Ser Val Gly His Gly Leu Asn Ala Ala Thr Gly
 465 470 475 480
 Glu Tyr Glu Asp Leu Leu Lys Ala Gly Val Ala Asp Pro Val Lys Val
 485 490 495
 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu
 500 505 510
 Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Thr Ala Ala Pro
 515 520 525
 Ala Ser Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe
 530 535 540

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ser Lys Leu Ile Glu Tyr Asp Glu Thr Ala Arg Arg Ala Met Glu
 1 5 10 15
 Val Gly Met Asp Lys Leu Ala Asp Thr Val Arg Val Thr Leu Gly Pro

20					25					30				
Arg Gly	Arg His	Val Val	Leu Ala	Lys Ala	Phe Gly	Gly Gly	Pro Thr	Val						
35			40			45								
Thr Asn	Asp Gly	Val Thr	Val Ala	Arg Glu	Ile Glu	Leu Glu	Asp Pro							
50			55		60									
Phe Glu	Asp Leu	Gly Ala	Gln Leu	Val Lys	Ser Val	Ala Thr	Lys Thr							
65		70		75			80							
Asn Asp	Val Ala	Gly Asp	Gly Thr	Thr Thr	Ala Thr	Ile Leu	Ala Gln							
		85		90			95							
Ala Leu	Ile Lys	Gly Gly	Leu Arg	Leu Val	Ala Ala	Gly Val	Asn Pro							
	100		105			110								
Ile Ala	Leu Gly	Val Gly	Ile Gly	Lys Ala	Ala Asp	Ala Val	Ser Glu							
	115		120		125									
Ala Leu	Leu Ala	Ser Ala	Thr Pro	Val Ser	Gly Lys	Thr Gly	Ile Ala							
130			135		140									
Gln Val	Ala Thr	Val Ser	Ser Arg	Asp Glu	Gln Ile	Gly Asp	Leu Val							
145		150		155			160							
Gly Glu	Ala Met	Ser Lys	Val Gly	His Asp	Gly Val	Val Ser	Val Glu							
		165		170			175							
Glu Ser	Ser Thr	Leu Gly	Thr Glu	Leu Glu	Phe Thr	Glu Gly	Ile Gly							
		180		185		190								
Phe Asp	Lys Gly	Phe Leu	Ser Ala	Tyr Phe	Val Thr	Asp Phe	Asp Asn							
	195		200		205									
Gln Gln	Ala Val	Leu Glu	Asp Ala	Leu Ile	Leu Leu	His Gln	Asp Lys							
210			215		220									
Ile Ser	Ser Leu	Pro Asp	Leu Leu	Pro Leu	Leu Glu	Lys Val	Ala Gly							
225		230		235			240							
Thr Gly	Lys Pro	Leu Leu	Ile Val	Ala Glu	Asp Val	Glu Gly	Glu Ala							
		245		250		255								
Leu Ala	Thr Leu	Val Val	Asn Ala	Ile Arg	Lys Thr	Leu Lys	Ala Val							
		260		265		270								
Ala Val	Lys Gly	Pro Tyr	Phe Gly	Asp Arg	Arg Lys	Ala Phe	Leu Glu							
	275		280		285									
Asp Leu	Ala Val	Val Thr	Gly Gly	Gln Val	Val Asn	Pro Asp	Ala Gly							
290			295		300									
Met Val	Leu Arg	Glu Val	Gly Leu	Glu Val	Leu Gly	Ser Ala	Arg Arg							
305		310		315			320							
Val Val	Val Ser	Lys Asp	Asp Thr	Val Ile	Val Asp	Gly Gly	Gly Thr							
		325		330		335								

Ala Glu Ala Val Ala Asn Arg Ala Lys His Leu Arg Ala Glu Ile Asp
340 345 350

Lys Ser Asp Ser Asp Trp Asp Arg Glu Lys Leu Gly Glu Arg Leu Ala
355 360 365

Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu
370 375 380

Thr Ala Leu Lys Glu Arg Lys Glu Ser Val Glu Asp Ala Val Ala Ala
385 390 395 400

Ala Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Ala Ser
405 410 415

Leu Ile His Gln Ala Arg Lys Ala Leu Thr Glu Leu Arg Ala Ser Leu
420 425 430

Thr Gly Asp Glu Val Leu Gly Val Asp Val Phe Ser Glu Ala Leu Ala
435 440 445

Ala Pro Leu Phe Trp Ile Ala Ala Asn Ala Gly Leu Asp Gly Ser Val
450 455 460

Val Val Lys Lys Val Ser Glu Leu Pro Ala Gly His Gly Leu Asn Val
465 470 475 480

Asn Thr Leu Ser Tyr Gly Asp Leu Ala Ala Asp Gly Val Ile Asp Pro
485 490 495

Val Lys Val Thr Arg Ser Ala Val Leu Asn Ala Ser Ser Val Ala Arg
500 505 510

Met Val Leu Thr Thr Glu Thr Val Val Val Asp Lys Pro Ala Lys Ala
515 520 525

Glu Asp His Asp His His His Gly His Ala His
530 535

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Ala Lys Asp Val Gln Phe Gly Asn Glu Val Arg Gln Lys Met
1 5 10 15

Val Asn Gly Val Asn Ile Leu Ala Asn Ala Val Arg Val Thr Leu Gly

20

25

30

Pro Lys Gly Arg Asn Val Val Val Asp Arg Ala Phe Gly Gly Pro His
 35 40 45
 Ile Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Lys Asp
 50 55 60
 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
 65 70 75 80
 Thr Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
 85 90 95
 Gln Ser Ile Val Ala Glu Gly Met Lys Tyr Val Thr Ala Gly Met Asn
 100 105 110
 Pro Thr Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Ala Ala Leu Val
 115 120 125
 Glu Glu Leu Lys Asn Ile Ala Lys Pro Cys Asp Thr Ser Lys Glu Ile
 130 135 140
 Ala Gln Val Gly Ser Ile Ser Ala Asn Ser Asp Glu Gln Val Gly Ala
 145 150 155 160
 Ile Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr
 165 170 175
 Val Glu Asp Gly Lys Ser Leu Glu Asn Glu Leu Asp Val Val Glu Gly
 180 185 190
 Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asp Ala
 195 200 205
 Glu Lys Gln Ile Ala Gly Leu Asp Asn Pro Phe Val Leu Leu Phe Asp
 210 215 220
 Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu Pro Val Leu Glu Gln Val
 225 230 235 240
 Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
 245 250 255
 Glu Ala Leu Ala Thr Leu Val Val Asn Asn Ile Arg Gly Ile Leu Lys
 260 265 270
 Thr Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
 275 280 285
 Leu Gln Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
 290 295 300
 Val Gly Leu Ser Leu Glu Lys Ala Thr Leu Asp Asp Leu Gly Gln Ala
 305 310 315 320
 Lys Arg Ile Glu Ile Gly Lys Glu Asn Thr Thr Ile Ile Asp Gly Phe
 325 330 335

Gly Asp Ala Ala Gln Ile Glu Ala Arg Val Ala Glu Ile Arg Gln Gln
 340 345 350
 Ile Glu Thr Ala Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg
 355 360 365
 Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
 370 375 380
 Thr Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Glu Asp Ala Leu
 385 390 395 400
 His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
 405 410 415
 Val Ala Leu Leu Arg Ala Arg Ala Ala Leu Glu Asn Leu His Thr Gly
 420 425 430
 Asn Ala Asp Gln Asp Ala Gly Val Gln Ile Val Leu Arg Ala Val Glu
 435 440 445
 Ser Pro Leu Arg Gln Ile Val Ala Asn Ala Gly Gly Glu Pro Ser Val
 450 455 460
 Val Val Asn Lys Val Leu Glu Gly Lys Gly Asn Tyr Gly Tyr Asn Ala
 465 470 475 480
 Gly Ser Gly Glu Tyr Gly Asp Met Ile Glu Met Gly Val Leu Asp Pro
 485 490 495
 Ala Lys Val Thr Arg Ser Ala Leu Gln His Ala Ala Ser Ile Ala Gly
 500 505 510
 Leu Met Leu Thr Thr Asp Cys Met Ile Ala Glu Ile Pro Glu Glu Lys
 515 520 525
 Pro Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Met
 530 535 540
 Glx
 545

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Val Lys Gln Leu Lys Phe Ser Glu Asp Ala Arg Gln Ala Met Leu

1 5 10 15
 Arg Gly Val Asp Gln Leu Ala Asn Ala Val Lys Val Thr Ile Gly Pro
 20 25 30
 Lys Gly Arg Asn Val Val Leu Asp Lys Glu Phe Thr Ala Pro Leu Ile
 35 40 45
 Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
 50 55 60
 Tyr Glu Asn Met Gly Ala Lys Leu Val Gln Glu Val Ala Asn Lys Thr
 65 70 75 80
 Asn Glu Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
 85 90 95
 Ala Met Ile Gln Glu Gly Leu Lys Asn Val Thr Ser Gly Ala Asn Pro
 100 105 110
 Val Gly Leu Arg Gln Gly Ile Asp Lys Ala Val Lys Val Ala Val Glu
 115 120 125
 Ala Leu His Glu Asn Ser Gln Lys Val Glu Asn Lys Asn Glu Ile Ala
 130 135 140
 Gln Val Gly Ala Ile Ser Ala Ala Asp Glu Glu Ile Gly Arg Tyr Ile
 145 150 155 160
 Ser Glu Ala Thr Glu Lys Val Gly Asn Asp Gly Val Ile Thr Ile Ile
 165 170 175
 Thr Ile Glu Glu Ser Asn Arg Leu Asn Thr Glu Leu Glu Leu Gly Met
 180 185 190
 Gln Phe Asp Arg Gly Tyr Gln Ser Pro Tyr Met Val Thr Asp Ser Asp
 195 200 205
 Lys Met Val Ala Glu Leu Glu Arg Pro Tyr Ile Leu Val Thr Asp Lys
 210 215 220
 Lys Ile Ser Ser Phe Gln Asp Ile Leu Pro Leu Leu Glu Gln Val Val
 225 230 235 240
 Gln Ser Asn Arg Pro Ile Leu Ile Val Ala Asp Glu Val Glu Gly Asp
 245 250 255
 Ala Leu Thr Asn Ile Val Leu Asn Arg Met Arg Gly Thr Phe Thr Ala
 260 265 270
 Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu
 275 280 285
 Glu Asp Leu Ala Ile Leu Thr Gly Ala Gln Val Ile Thr Asp Asp Leu
 290 295 300
 Gly Leu Asp Leu Lys Asp Ala Ser Ile Asp Met Leu Gly Thr Ala Ser
 305 310 315 320

Lys Val Glu Val Thr Lys Asp Asn Thr Thr Val Val Asp Gly Asp Gly
 325 330 335
 Asp Glu Asn Ser Ile Asp Ala Arg Val Ser Gln Leu Lys Ser Gln Ile
 340 345 350
 Glu Glu Thr Glu Ser Asp Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu
 355 360 365
 Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser
 370 375 380
 Glu Thr Glu Leu Lys Glu Arg Lys Leu Arg Ile Glu Asp Ala Leu Asn
 385 390 395 400
 Ser Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Thr
 405 410 415
 Ala Leu Val Asn Val Tyr Gln Lys Val Ser Glu Asn Glu Ala Glu Gly
 420 425 430
 Asp Ile Glu Thr Gly Val Asn Ile Val Leu Lys Ala Leu Thr Ala Pro
 435 440 445
 Val Arg Gln Ile Ala Glu Asn Ala Gly Leu Glu Gly Ser Val Ile Val
 450 455 460
 Glu Arg Leu Lys Asn Ala Glu Pro Gly Val Gly Phe Asn Gly Ala Thr
 465 470 475 480
 Asn Glu Trp Val Asn Met Leu Arg Arg Gly Ile Val Asp Pro Thr Lys
 485 490 495
 Val Thr Arg Ser Ala Leu Gln His Ala Ala Ser Val Ala Ala Met Phe
 500 505 510
 Leu Thr Thr Glu Ala Val Val Ala Ser Ile Pro Glu Lys Asn Asn Asp
 515 520 525
 Gln Pro Asn Met Gly Gly Met Pro Gly Met Met
 530 535

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Lys Ser Ile Ile Tyr Asn Asp Glu Ala Arg Arg Ala Leu Glu

1	5	10	15
Arg Gly Met Asp Ile Leu Ala Glu Ala Val Ala Val Thr Leu Gly Pro	20	25	30
Lys Gly Arg Asn Val Val Leu Glu Lys Lys Phe Gly Ser Pro Gln Ile	35	40	45
Ile Asn Asp Gly Ile Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His	50	55	60
Val Glu Asn Thr Gly Val Ser Leu Ile Arg Gln Ala Ala Ser Lys Thr	65	70	75
Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala His	85	90	95
Ala Ile Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro	100	105	110
Ile Ser Leu Lys Arg Gly Ile Asp Lys Ala Thr Asp Phe Leu Val Ala	115	120	125
Arg Ile Lys Glu His Ala Gln Pro Val Gly Asp Ser Lys Ala Ile Ala	130	135	140
Gln Val Gly Ala Ile Ser Ala Gly Asn Asp Glu Glu Val Gly Gln Met	145	150	155
Ile Ala Asn Ala Met Asp Lys Val Gly Gln Glu Gly Val Ile Ser Leu	165	170	175
Glu Glu Gly Lys Ser Met Thr Thr Glu Leu Glu Ile Thr Glu Gly Met	180	185	190
Arg Phe Asp Lys Gly Tyr Ile Ser Pro Tyr Phe Val Thr Asp Ala Glu	195	200	205
Arg Met Glu Ala Val Leu Glu Asp Pro Arg Ile Leu Ile Thr Asp Lys	210	215	220
Lys Ile Asn Leu Val Gln Asp Leu Val Pro Ile Leu Glu Gln Val Ala	225	230	235
Arg Gln Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Lys Glu	245	250	255
Ala Leu Ala Thr Leu Val Val Asn Arg Leu Arg Gly Val Leu Asn Val	260	265	270
Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Gln Met Leu	275	280	285
Glu Asp Ile Ala Thr Leu Thr Gly Gly Gln Val Ile Ser Glu Asp Ala	290	295	300
Gly Leu Lys Leu Glu Ser Ala Thr Val Asp Ser Leu Gly Ser Ala Arg	305	310	315
			320

Arg Ile Asn Ile Thr Lys Asp Asn Thr Thr Ile Val Ala Glu Gly Asn
 325 330 335
 Glu Ala Ala Val Lys Ser Arg Cys Glu Gln Ile Arg Arg Gln Ile Glu
 340 345 350
 Glu Thr Asp Ser Ser Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu
 370 375 380
 Thr Glu Met Lys Asp Arg Lys Leu Arg Leu Glu Asp Ala Ile Asn Ala
 385 390 395 400
 Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Thr Thr
 405 410 415
 Leu Ala His Leu Ala Pro Gln Leu Glu Asp Trp Ala Thr Gly Asn Leu
 420 425 430
 Lys Asp Glu Glu Leu Thr Gly Ala Leu Ile Val Ala Arg Ala Leu Pro
 435 440 445
 Ala Pro Leu Lys Arg Ile Ala Glu Asn Ala Gly Gln Asn Gly Ala Val
 450 455 460
 Ile Ser Glu Arg Val Lys Glu Lys Glu Phe Asn Val Gly Tyr Asn Ala
 465 470 475 480
 Ala Ser Leu Glu Tyr Val Asp Met Leu Ala Ala Gly Ile Val Asp Pro
 485 490 495
 Ala Lys Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly
 500 505 510
 Met Val Leu Thr Thr Glu Cys Ile Val Val Asp Lys Pro Glu Lys Glu
 515 520 525
 Lys Ala Pro Ala Gly Ala Pro Gly Gly Asp Phe Asp Tyr
 530 535 540

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ser Lys Leu Ile Ser Phe Lys Asp Glu Ser Arg Arg Ser Leu Glu

1	5	10	15
Ala Gly Ile	Asn Ala Leu Ala Asp	Ala Val Arg Ile Thr	Leu Gly Pro
	20	25	30
Lys Gly Arg	Asn Val Leu Leu Glu	Lys Gln Tyr Gly	Ala Pro Gln Ile
	35	40	45
Val Asn Asp	Gly Ile Thr Val Ala Lys	Glu Ile Glu	Leu Ser Asn Pro
	50	55	60
Glu Glu Asn	Ala Gly Ala Lys Leu Ile	Gln Glu Val	Ala Ser Lys Thr
	65	70	75
Lys Glu Ile	Ala Gly Asp Gly Thr Thr	Thr Ala Thr	Ile Ile Ala Gln
	85	90	95
Ala Leu Val	Arg Glu Gly Leu Arg Asn	Val Ala Ala Gly	Ala Asn Pro
	100	105	110
Val Ala Leu	Arg Arg Gly Ile Glu Lys	Val Thr Thr Phe	Leu Val Gln
	115	120	125
Glu Ile Glu	Ala Val Ala Lys Pro	Val Glu Gly Ser	Ala Ile Ala Gln
	130	135	140
Val Ala Thr	Val Ser Ser Gly Asn Asp	Pro Glu Val Gly	Ala Met Ile
	145	150	155
Ala Asp Ala	Met Asp Lys Val Thr Lys	Asp Gly Val Ile	Thr Val Glu
	165	170	175
Glu Ser Lys	Ser Leu Asn Thr Glu Leu	Glu Val Val Glu	Gly Met Gln
	180	185	190
Ile Asp Arg	Gly Tyr Ile Ser Pro Tyr	Phe Ile Thr Asp	Ser Asp Arg
	195	200	205
Gln Leu Val	Glu Phe Asp Asn Pro Leu	Ile Leu Ile Thr	Asp Lys Lys
	210	215	220
Ile Ser Ala	Ile Ala Glu Leu Val Pro	Val Leu Glu Ala	Val Ala Arg
	225	230	235
Ala Gly Arg	Pro Leu Leu Ile Ile Ala	Glu Asp Ile Glu	Gly Glu Ala
	245	250	255
Leu Ala Thr	Leu Val Val Asn Lys Ala	Arg Gly Val Leu	Asn Val Ala
	260	265	270
Ala Ile Lys	Ala Pro Ala Phe Gly Asp	Arg Arg Lys Ala	Val Leu Gln
	275	280	285
Asp Ile Ala	Ile Leu Thr Gly Gly Ser	Val Ile Ser Glu	Asp Ile Gly
	290	295	300
Leu Ser Leu	Asp Thr Val Ser Leu Asp	Gln Leu Gly Gln	Ala Val Lys
	305	310	315
			320

Ala Thr Leu Glu Lys Asp Asn Thr Ile Leu Val Ala Gly Ala Asp Lys
325 330 335

Arg Ala Ser Ala Gly Val Lys Glu Arg Ile Glu Gln Leu Arg Lys Glu
340 345 350

Tyr Ala Ala Ser Asp Ser Asp Tyr Asp Lys Glu Lys Ile Gln Glu Arg
355 360 365

Ile Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
370 375 380

Thr Glu Thr Glu Leu Lys Asp Arg Lys Leu Arg Ile Glu Asp Ala Leu
385 390 395 400

Asn Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly
405 410 415

Thr Thr Leu Ile Arg Leu Ala Gly Lys Ile Glu Ser Phe Lys Ala Gln
420 425 430

Leu Ser Asn Asp Glu Glu Arg Val Ala Ala Asp Ile Ile Ala Lys Ala
435 440 445

Leu Glu Ala Pro Leu His Gln Leu Ala Ser Asn Ala Gly Val Glu Gly
450 455 460

Ser Val Ile Val Glu Lys Val Lys Glu Ala Thr Gly Asn Gln Gly Tyr
465 470 475 480

Asn Val Ile Thr Gly Lys Ile Glu Asp Leu Ile Ala Ala Gly Ile Ile
485 490 495

Asp Pro Ala Lys Val Val Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile
500 505 510

Ala Gly Met Val Leu Thr Thr Glu Ala Leu Val Val Glu Lys Pro Glu
515 520 525

Pro Ala Ala Pro Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly
530 535 540

Gly Met Gly Gly Met Gly Met Met
545 550

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Ala Lys Thr Ile Ala Phe Asp Lys Lys Ala Arg Arg Gly Leu Glu
1 5 10 15

Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro
20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
35 40 45

Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
50 55 60

Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
65 70 75 80

Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
85 90 95

Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
100 105 110

Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Ala Val Thr Glu
115 120 125

His Leu Leu Lys Ala Ala Lys Glu Val Glu Thr Lys Asp Gln Ile Ala
130 135 140

Ala Thr Ala Gly Ile Ser Ala Gly Asp Pro Ala Ile Gly Glu Leu Ile
145 150 155 160

Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr Val Glu
165 170 175

Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
180 185 190

Phe Asp Lys Gly Phe Ile Ser Gly Tyr Phe Ala Thr Asp Ala Glu Arg
195 200 205

Gln Glu Ala Val Leu Glu Asp Pro Tyr Val Leu Leu Val Ser Gly Lys
210 215 220

Ile Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln
225 230 235 240

Ser Gly Lys Pro Leu Ala Ile Ile Ala Glu Asp Val Glu Gly Glu Ala
245 250 255

Leu Val Thr Leu Ile Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val
260 265 270

Ala Ile Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln
275 280 285

Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Ile Gly
290 295 300

Leu Ser Leu Asp Thr Ala Gly Leu Glu Val Leu Gly Gln Ala Arg Gln
 305 310 315 320
 Val Val Val Thr Lys Asp Glu Thr Thr Ile Val Asp Gly Ala Gly Ser
 325 330 335
 Lys Glu Gln Ile Ala Gly Arg Val Ser Gln Ile Arg Ala Glu Ile Glu
 340 345 350
 Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu
 370 375 380
 Asp Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala
 385 390 395 400
 Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Ser Ser Leu
 405 410 415
 Ala Gln Ser Gly Thr Val Phe Asp Ser Xaa Ala Leu Glu Gly Asp Glu
 420 425 430
 Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Asp Ala Pro Val Lys
 435 440 445
 Gln Ile Ala Val Asn Ala Gly Leu Glu Pro Gly Val Val Ala Glu Lys
 450 455 460
 Val Arg Asn Ser Pro Ala Gly Thr Gly Leu Asn Ala Ala Thr Gly Val
 465 470 475 480
 Tyr Glu Asp Leu Leu Ala Ala Gly Ile Asn Asp Pro Val Lys Val Thr
 485 490 495
 Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Ala Leu Phe Leu Thr
 500 505 510
 Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Ala Gly Ala Pro Val
 515 520 525
 Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe
 530 535

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Val Ser Phe Leu Ser Ser Ser Val Ser Arg Leu Pro Leu Arg Ile
1 5 10 15

Ala Gly Arg Arg Ile Pro Gly Arg Phe Ala Val Pro Gln Val Arg Thr
20 25 30

Tyr Ala Lys Asp Leu Lys Phe Gly Val Asp Ala Arg Ala Ser Leu Leu
35 40 45

Thr Gly Val Asp Thr Leu Ala Arg Ala Val Ser Val Thr Leu Gly Pro
50 55 60

Lys Gly Arg Asn Val Leu Ile Asp Gln Pro Phe Gly Ser Pro Lys Ile
65 70 75 80

Thr Lys Asp Gly Val Thr Val Ala Arg Ser Val Ser Leu Lys Asp Lys
85 90 95

Phe Glu Asn Leu Gly Ala Arg Leu Val Gln Asp Val Ala Ser Lys Thr
100 105 110

Asn Glu Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Arg
115 120 125

Ala Ile Phe Ser Glu Thr Val Arg Asn Val Ala Ala Gly Cys Asn Pro
130 135 140

Met Asp Leu Arg Arg Gly Ile Gln Leu Ala Val Asp Asn Val Val Glu
145 150 155 160

Phe Leu Gln Ala Asn Lys Arg Asp Ile Thr Thr Ser Glu Glu Ile Ser
165 170 175

Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Thr His Ile Gly Glu Leu
180 185 190

Leu Ala Lys Ala Met Glu Arg Val Gly Lys Glu Gly Val Ile Thr Val
195 200 205

Lys Glu Gly Arg Thr Ile Ser Asp Glu Leu Glu Val Thr Glu Gly Met
210 215 220

Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asp Val Lys
225 230 235 240

Ser Gln Lys Val Glu Phe Glu Asn Pro Leu Ile Leu Leu Ser Glu Lys
245 250 255

Lys Val Ser Ala Val Gln Asp Ile Leu Pro Ser Leu Glu Leu Ala Ala
260 265 270

Gln Gln Arg Arg Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu
275 280 285

Ala Leu Ala Ala Cys Ile Leu Asn Lys Leu Arg Gly Gln Leu Gln Val
290 295 300

Val Ala Ile Lys Ala Pro Gly Phe Gly Asp Asn Arg Arg Asn Met Leu
 305 310 315 320
 Gly Asp Leu Ala Val Leu Thr Asp Ser Ala Val Phe Asn Asp Glu Ile
 325 330 335
 Asp Val Ser Ile Glu Lys Ala Gln Pro His His Leu Gly Ser Cys Gly
 340 345 350
 Ser Val Thr Val Thr Lys Glu Asp Thr Ile Ile Met Lys Gly Ala Gly
 355 360 365
 Asp His Val Lys Val Asn Asp Arg Cys Glu Gln Ile Arg Gly Val Met
 370 375 380
 Ala Asp Pro Asn Leu Thr Glu Ser Glu Lys Glu Lys Leu Gln Glu Arg
 385 390 395 400
 Leu Ala Lys Leu Ser Gly Gly Ile Ala Val Ile Lys Val Gly Ala Ser
 405 410 415
 Ser Glu Val Glu Val Asn Glu Lys Lys Asp Arg Ile Val Asp Ala Leu
 420 425 430
 Asn Ala Val Lys Ala Ala Val Ser Glu Gly Val Leu Pro Gly Ala Gly
 435 440 445
 Thr Ser Phe Val Lys Ala Ser Leu Arg Leu Gly Asp Ile Pro Thr Asn
 450 455 460
 Asn Phe Asp Gln Lys Leu Gly Val Glu Ile Val Arg Lys Ala Ile Thr
 465 470 475 480
 Arg Pro Ala Gln Thr Ile Leu Glu Asn Ala Gly Leu Glu Gly Asn Leu
 485 490 495
 Ile Val Gly Lys Leu Lys Glu Leu Tyr Gly Lys Glu Phe Asn Ile Gly
 500 505 510
 Tyr Asp Ile Ala Lys Asp Arg Phe Val Asp Leu Asn Glu Ile Gly Val
 515 520 525
 Leu Asp Pro Leu Lys Val Val Arg Thr Gly Leu Val Asp Ala Ser Gly
 530 535 540
 Val Ala Ser Leu Met Gly Thr Thr Glu Cys Ala Ile Val Asp Ala Pro
 545 550 555 560
 Glu Glu Ser Lys Ala Pro Ala Gly Pro Pro Gly Met Gly Gly Met Gly
 565 570 575
 Gly Met Pro Gly Met Met
 580

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Leu Arg Ser Ser Val Val Arg Ser Arg Ala Thr Leu Arg Pro Leu
 1 5 10 15

Leu Arg Arg Ala Tyr Ser Ser His Lys Glu Leu Lys Phe Gly Val Glu
 20 25 30

Gly Arg Ala Ser Leu Leu Lys Gly Val Glu Thr Leu Ala Glu Ala Val
 35 40 45

Ala Ala Thr Leu Gly Pro Lys Gly Arg Asn Val Leu Ile Glu Gln Pro
 50 55 60

Phe Gly Pro Pro Lys Ile Thr Lys Asp Gly Val Thr Val Ala Lys Ser
 65 70 75 80

Ile Val Leu Lys Asp Lys Phe Glu Asn Met Gly Ala Lys Leu Leu Gln
 85 90 95

Glu Val Ala Ser Lys Thr Asn Glu Ala Ala Gly Asp Gly Thr Thr Ser
 100 105 110

Ala Thr Val Leu Gly Arg Ala Ile Phe Thr Glu Ser Val Lys Asn Val
 115 120 125

Ala Ala Gly Cys Asn Pro Met Asp Leu Arg Arg Gly Ser Gln Val Ala
 130 135 140

Val Glu Lys Val Ile Glu Phe Leu Ser Ala Asn Lys Lys Glu Ile Thr
 145 150 155 160

Thr Ser Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp
 165 170 175

Ser His Val Gly Lys Leu Leu Ala Ser Ala Met Glu Lys Val Gly Lys
 180 185 190

Glu Gly Val Ile Thr Ile Arg Glu Gly Arg Thr Leu Glu Asp Glu Leu
 195 200 205

Glu Val Thr Glu Gly Met Arg Phe Asp Arg Gly Phe Ile Ser Pro Tyr
 210 215 220

Phe Ile Thr Asp Pro Lys Ser Ser Lys Val Glu Phe Glu Lys Pro Leu
 225 230 235 240

Leu Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Asp Ile Leu Pro
 245 250 255

Ala Leu Glu Ile Ser Asn Gln Ser Arg Arg Pro Leu Leu Ile Ile Ala
 260 265 270
 Glu Asp Val Asp Gly Glu Ala Leu Ala Ala Cys Ile Leu Asn Lys Leu
 275 280 285
 Arg Gly Gln Val Lys Val Cys Ala Val Lys Ala Pro Gly Phe Gly Asp
 290 295 300
 Asn Arg Lys Asn Thr Ile Gly Asp Ile Ala Val Leu Thr Gly Gly Thr
 305 310 315 320
 Val Phe Thr Glu Glu Leu Asp Leu Lys Pro Glu Gln Cys Thr Ile Glu
 325 330 335
 Asn Leu Gly Ser Cys Asp Ser Ile Thr Val Thr Lys Glu Asp Thr Val
 340 345 350
 Ile Leu Asn Gly Ser Gly Pro Lys Glu Ala Ile Gln Glu Arg Ile Glu
 355 360 365
 Gln Ile Lys Gly Ser Ile Asp Ile Thr Thr Thr Asn Ser Tyr Glu Lys
 370 375 380
 Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val
 385 390 395 400
 Ile Arg Val Gly Gly Ala Ser Glu Val Glu Val Gly Glu Lys Lys Asp
 405 410 415
 Arg Tyr Asp Asp Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly
 420 425 430
 Ile Leu Pro Gly Gly Gly Thr Ala Leu Val Lys Ala Ser Arg Val Leu
 435 440 445
 Asp Glu Val Val Val Asp Asn Phe Asp Gln Lys Leu Gly Val Asp Ile
 450 455 460
 Ile Arg Lys Ala Ile Thr Arg Pro Ala Lys Gln Ile Ile Glu Asn Ala
 465 470 475 480
 Gly Glu Glu Gly Ser Val Ile Ile Gly Lys Leu Ile Asp Glu Tyr Gly
 485 490 495
 Asp Asp Phe Ala Lys Gly Tyr Asp Ala Ser Lys Ser Glu Tyr Thr Asp
 500 505 510
 Met Leu Ala Thr Gly Ile Ile Asp Pro Phe Lys Val Val Arg Ser Gly
 515 520 525
 Leu Val Asp Ala Ser Gly Val Ala Ser Leu Leu Ala Thr Thr Glu Val
 530 535 540
 Ala Ile Val Asp Ala Pro Glu Pro Pro Ala Ala Ala Gly Ala Gly Gly
 545 550 555 560

Met Pro Gly Gly Met Pro Gly Met Pro Gly Met Met
565 570

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ile Ser Thr Leu Arg Gly Lys Ile Phe Asn Asn Gly Ser Asn Arg
1 5 10 15

Asn Lys Cys Val Ser Ile Leu Ser Asn Ile Gln Lys Arg Asn Ile Ser
20 25 30

Lys Asp Ile Arg Phe Gly Ser Asp Ala Arg Thr Ala Met Leu Thr Gly
35 40 45

Cys Asn Lys Leu Ala Asp Ala Val Ser Val Thr Leu Gly Pro Lys Gly
50 55 60

Arg Asn Val Ile Ile Glu Gln Ser Phe Gly Ser Pro Lys Ile Thr Lys
65 70 75 80

Asp Gly Val Thr Val Ala Lys Ser Ile Glu Phe Asn Asn Lys Leu Ala
85 90 95

Asn Leu Gly Ala Gln Met Val Lys Gln Val Ala Ala Asn Thr Asn Gly
100 105 110

Lys Ala Gly Asp Gly Thr Thr Thr Ala Thr Ile Leu Ala Arg Ser Ile
115 120 125

Phe Gln Gln Gly Cys Lys Ala Val Asp Ser Gly Met Asn Pro Met Asp
130 135 140

Leu Leu Arg Gly Ile Asn Lys Gly Val Glu Lys Val Leu Glu Tyr Leu
145 150 155 160

Asn Ser Ile Lys Lys Asp Val Thr Thr Thr Glu Glu Ile Phe Asn Val
165 170 175

Ala Ser Ile Ser Asn Gly Asp Lys Asn Ile Gly Gln Leu Ile Ala Asp
180 185 190

Thr Met Lys Lys Val Gly Lys Glu Gly Thr Ile Thr Val Thr Glu Gly
195 200 205

Lys Thr Leu Gln His Glu Leu Glu Ile Val Glu Gly Ile Lys Phe Asp
210 215 220

Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Asn Ser Gln Lys Val Glu
 225 230 235 240
 Leu Asp Lys Pro Tyr Ile Leu Ile His Glu Lys Lys Ile Ser Thr Val
 245 250 255
 Lys Ser Leu Leu Pro Val Leu Glu His Val Leu Gln Asn Gln Ser Ser
 260 265 270
 Leu Leu Val Ile Ala Glu Asp Val Asp Ser Asp Ala Leu Ala Thr Leu
 275 280 285
 Ile Val Asn Lys Leu Arg Leu Gly Leu Lys Ile Cys Ala Val Lys Ala
 290 295 300
 Pro Gly Phe Gly Glu His Arg Lys Ala Leu Ile His Asp Ile Ala Val
 305 310 315 320
 Met Thr Gly Ala Lys Val Ile Thr Glu Glu Thr Gly Leu Lys Leu Asp
 325 330 335
 Asp Pro Gln Val Val Ser Tyr Leu Gly Lys Ala Lys Ser Ile Asn Val
 340 345 350
 Thr Lys Asp Ser Thr Leu Ile Met Glu Gly Glu Gly Lys Lys Glu Glu
 355 360 365
 Ile Asn Glu Arg Cys Glu Ser Ile Arg Asn Ala Ile Lys Met Asn Thr
 370 375 380
 Ser Asp Tyr Glu Lys Glu Lys Leu Gln Glu Arg Leu Ala Lys Ile Thr
 385 390 395 400
 Gly Gly Val Ala Leu Ile Lys Val Gly Gly Ile Ser Glu Val Glu Val
 405 410 415
 Asn Glu Ile Lys Asp Arg Ile Gln Asp Ala Leu Cys Ala Thr Lys Ala
 420 425 430
 Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Ser Ala Leu Leu Phe
 435 440 445
 Ala Ser Lys Glu Leu Asp Ser Val Gln Thr Asp Asn Tyr Asp Gln Arg
 450 455 460
 Val Gly Val Asn Ile Ile Lys Asp Ala Cys Lys Ala Pro Ile Lys Gln
 465 470 475 480
 Ile Ala Glu Asn Ala Gly His Glu Gly Ser Val Val Ala Gly Asn Ile
 485 490 495
 Leu Lys Asp Lys Asn Ser Asn Ile Gly Phe Asn Ala Gln Glu Gly Lys
 500 505 510
 Tyr Val Asp Met Ile Glu Ser Gly Ile Ile Asp Pro Thr Lys Val Val
 515 520 525

Lys Thr Ala Ile Ser Asp Ala Ala Ser Ile Ala Ser Leu Met Thr Thr
530 535 540

Thr Glu Val Ala Ile Val Asp Phe Lys Asp Ser Lys Asn Glu Glu Ser
545 550 555 560

Ser Gln His Met Asn Ser Val Asn Ser Met Gly Asp Met Gly Gly Met
565 570 575

Tyr

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Thr Asn Val Val Val Ser Gly Glu Gln Leu Gln Gln Ala Phe Arg
1 5 10 15

Glu Val Ala Ala Val Ile Asp Ser Thr Val Ala Val Thr Ala Gly Pro
20 25 30

Arg Gly Lys Thr Val Gly Ile Asn Lys Pro Tyr Gly Ala Pro Glu Ile
35 40 45

Thr Lys Asp Gly Tyr Lys Val Met Lys Gly Ile Lys Pro Glu Lys Pro
50 55 60

Leu Asn Ala Ala Ile Thr Ser Ile Phe Ala Gln Ser Cys Ser Gln Cys
65 70 75 80

Asn Asp Lys Val Gly Asp Gly Thr Thr Thr Cys Ser Ile Leu Thr Ser
85 90 95

Gly Met Ile Val Glu Ala Ser Lys Ser Ile Ala Ala Gly Asn Asp Arg
100 105 110

Ile Ser Ile Lys Asn Gly Met Gln Lys Ala Lys Asp Val Val Leu Lys
115 120 125

Glu Val Ala Ser Met Ala Arg Thr Ile Ser Leu Glu Lys Ile Asp Glu
130 135 140

Val Ala Gln Val Ala Ile Ile Ser Ala Asn Gly Asp Arg Ser Ile Gly
145 150 155 160

Ser Asn Ile Ala Asp Ala Val Lys Lys Val Gly Lys Glu Gly Val Ile
165 170 175

Thr Val Glu Glu Ser Lys Gly Ser Lys Glu Leu Glu Val Glu Leu Thr
 180 185 190
 Thr Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Thr
 195 200 205
 Asn Asn Glu Lys Met Ile Val Glu Leu Asp Asp Pro Tyr Leu Leu Ile
 210 215 220
 Thr Glu Lys Lys Leu Asn Ile Ile Gln Pro Leu Leu Ser Ile Leu Glu
 225 230 235 240
 Ala Val Val Lys Ser Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile
 245 250 255
 Glu Gly Glu Ala Leu Ser Thr Leu Val Ile Asn Lys Leu Arg Gly Gly
 260 265 270
 Leu Lys Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys
 275 280 285
 Glu Met Leu Glu Asp Ile Ala Ala Leu Thr Asn Ala Lys Tyr Val Ile
 290 295 300
 Lys Asp Glu Leu Gly Ile Lys Met Glu Asp Leu Thr Leu Glu Asp Leu
 305 310 315 320
 Gly Ile Ala Lys Asn Val Lys Ile Thr Lys Asp Asn Thr Thr Ile Val
 325 330 335
 Ser Glu Asn Arg Val Thr Asp Arg Val Lys Ala Arg Ile Glu Gln Ile
 340 345 350
 Lys Ser Gln Ile Glu Ser Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu
 355 360 365
 Arg Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Leu Lys Val
 370 375 380
 Gly Gly Ala Thr Glu Leu Glu Val Lys Glu Arg Arg Asp Arg Val Glu
 385 390 395 400
 Asp Gln Leu His Ala Thr Arg Ala Ala Ile Glu Glu Gly Ile Val Pro
 405 410 415
 Gly Gly Gly Val Ala Leu Leu Tyr Ala Ser Ser Ala Leu Asp Lys Leu
 420 425 430
 Lys Gly Ala Asp Asp Glu Glu Gln Ile Gly Ile Asn Ile Ile Lys Lys
 435 440 445
 Val Leu Ser Val Pro Ile Lys Arg Leu Val Lys Asn Ala Gly Leu Glu
 450 455 460
 Ser Ala Val Ile Ile Asp Tyr Leu Ile Lys Gln Asn Asn Lys Glu Leu
 465 470 475 480

Ile	Tyr	Asn	Val	Glu	Ala	Met	Ser	Tyr	Ala	Asn	Ala	Phe	Ala	Ala	Gly	485	490	495
Val	Ile	Asp	Pro	Ala	Lys	Val	Val	Arg	Ile	Ala	Phe	Glu	Thr	Ala	Ile	500	505	510
Ser	Val	Ala	Ser	Val	Leu	Ile	Thr	Thr	Glu	Ser	Met	Ile	Val	Asp	Ile	515	520	525
Pro	Asn	Lys	Asp	Glu	Asn	Ala	Ser	Ser	Pro	Met	Gly	Ala	Gly	Gly	Met	530	535	540
Gly	Arg	Met	Asn	Asp	Phe											545	550	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Leu Arg Leu Ala Arg Lys Gly Leu Gln Thr Ala Val Val Arg Ser
1 5 10 15

Tyr Ala Lys Asp Val Lys Phe Gly Ala Glu Gly Arg Gln Ala Met Leu
20 25 30

Val Gly Val Asn Leu Leu Ala Asp Ala Val Ser Val Thr Met Gly Pro
35 40 45

Lys Gly Arg Asn Val Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Ile
50 55 60

Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys
65 70 75 80

Tyr Gln Asn Leu Gly Ala Lys Leu Ile Gln Asp Val Ala Asn Lys Ala
85 90 95

Asn Glu Glu Ala Gly Asp Gly Thr Thr Cys Ala Thr Val Leu Thr Arg
100 105 110

Ala Ile Ala Lys Glu Gly Phe Glu Arg His Ser Ser Arg Gly Asn Ala
115 120 125

Val Glu Ile Arg Arg Gly Val Met Asn Ala Val Glu Val Val Val Ala
130 135 140

Glu Leu Lys Lys Ile Ser Lys Lys Val Thr Thr Pro Glu Glu Ile Ala
145 150 155 160

Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Thr Val Val Gly Asn Leu
 165 170 175
 Ile Ser Asp Ala Met Lys Lys Val Gly Thr Thr Gly Val Ile Thr Val
 180 185 190
 Lys Asp Gly Lys Thr Leu Asn Asp Gln Leu Glu Leu Ile Glu Gly Met
 195 200 205
 Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Ser Ala Lys
 210 215 220
 Gly Ala Lys Val Glu Tyr Glu Lys Ala Leu Val Leu Leu Ser Glu Lys
 225 230 235 240
 Lys Ile Ser Gln Val Gln Asp Ile Val Pro Ala Leu Glu Leu Ala Asn
 245 250 255
 Lys Leu Arg Arg Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu
 260 265 270
 Ala Leu Thr Thr Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val
 275 280 285
 Val Ala Ile Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Ala Leu
 290 295 300
 Lys Asp Met Gly Ile Ala Thr Gly Ala Ser Ile Phe Gly Asp Glu Thr
 305 310 315 320
 Leu Asp Leu Arg Leu Glu Asp Ile Thr Ala Asn Asp Leu Gly Glu Val
 325 330 335
 Asp Glu Val Thr Ile Thr Lys Asp Asp Thr Leu Leu Leu Arg Gly Arg
 340 345 350
 Gly Asp Gln Thr Glu Ile Glu Lys Arg Ile Glu Glu Ile Thr Asp Glu
 355 360 365
 Ile Glu Arg Ser Thr Ser Asp Tyr Glu Lys Glu Lys Leu Asn Glu Arg
 370 375 380
 Leu Ala Lys Leu Ser Lys Gly Val Ala Val Leu Lys Ile Gly Gly Gly
 385 390 395 400
 Ser Glu Val Glu Val Gly Glu Lys Lys Asp Arg Val Thr Asp Ala Leu
 405 410 415
 Cys Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly
 420 425 430
 Val Ala Leu Leu Arg Ser Leu Thr Ala Leu Lys Asn Tyr Lys Ala Ala
 435 440 445
 Asn Glu Asp Gln Gln Ile Gly Val Asn Ile Val Lys Lys Ala Leu Thr
 450 455 460

Gln Pro Ile Ala Thr Ile Val Lys Asn Ala Gly Leu Glu Pro Ser Ser
 465 470 475 480
 Ile Ile Asp Glu Val Thr Gly Asn Ser Asn Thr Ser Tyr Gly Tyr Asp
 485 490 495
 Ala Leu Asn Gly Lys Phe Val Asp Met Phe Glu Ala Gly Ile Ile Asp
 500 505 510
 Pro Thr Lys Val Val Arg Thr Ala Leu Gln Asp Ala Ser Gly Val Ala
 515 520 525
 Ser Leu Leu Ala Thr Thr Glu Cys Val Val Thr Glu Ile Pro Lys Glu
 530 535 540
 Glu Ala Val Gly Gly Pro Ala Gly Gly Met Gly Gly Met Gly Gly Met
 545 550 555 560
 Gly Gly Met Gly Gly Met Gly Phe
 565

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Phe Arg Leu Pro Val Ser Leu Ala Arg Ser Ser Ile Ser Arg Gln
 1 5 10 15
 Leu Ala Met Arg Gly Tyr Ala Lys Asp Val Arg Phe Gly Pro Glu Val
 20 25 30
 Arg Ala Met Met Leu Gln Gly Val Asp Val Leu Ala Asp Ala Val Ala
 35 40 45
 Val Thr Met Gly Pro Lys Gly Arg Asn Val Ile Ile Glu Gln Ser Val
 50 55 60
 Gly Leu Ala Lys Ile Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile
 65 70 75 80
 Glu Leu Lys Asp Lys Phe Gln Asn Ile Gly Ala Lys Leu Val Gln Asp
 85 90 95
 Leu Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala
 100 105 110
 Thr Phe Leu Ala Arg Ala Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser
 115 120 125

Lys Gly Gly Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val
 130 135 140
 Glu Thr Val Lys Asp Asn Leu Lys Thr Met Ser Arg Pro Val Ser Thr
 145 150 155 160
 Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Arg
 165 170 175
 Glu Ile Gly Asn Gly Lys Val Ser Val Ser Glu Ala Met Lys Lys Val
 180 185 190
 Gly Arg Asp Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Thr Asp
 195 200 205
 Glu Leu Glu Val Ile Glu Gly Thr Met Arg Phe Asp Arg Gly Tyr Ile
 210 215 220
 Ser Pro Tyr Phe Ile Asn Ser Ser Lys Gly Ala Lys Val Glu Phe Gln
 225 230 235 240
 Asp Ala Leu Leu Leu Leu Ser Glu Lys Lys Ile Ser Ser Val Ala Glu
 245 250 255
 His His Ser Pro Leu Trp Arg Leu Ala Ser Arg Arg Thr Arg Lys Pro
 260 265 270
 Leu Val Ile Ile Ala Glu Asp Ile Asp Gly Glu Ala Leu Ser Thr Leu
 275 280 285
 Val Val Asn Arg Leu Lys Ile Gly Leu Gln Val Ala Ala Val Lys Ala
 290 295 300
 Pro Gly Phe Gly Asp Asn Arg Lys Ser Thr Leu Thr Asp Met Ala Thr
 305 310 315 320
 Ser Gly Gly Ile Val Phe Gly Asp Asp Val Ser Leu Val Lys Leu Glu
 325 330 335
 Asp Val Lys Val Ser Asp Leu Gly Gln Val Gly Glu Val Val Ile Thr
 340 345 350
 Lys Asp Asp Thr Leu Leu Leu Lys Gly Lys Gly Lys Lys Asp Asp Val
 355 360 365
 Leu Arg Arg Ala Asn Gln Ile Arg Thr Lys Ile Glu Asp Thr Thr Ser
 370 375 380
 Glu Tyr Glu Lys Glu Lys Leu Gln Glu Arg Leu Ala Arg Leu Ala Ser
 385 390 395 400
 Gly Val Ala Leu Arg Val Gly Gly Ser Ser Glu Val Glu Val Asn Glu
 405 410 415
 Lys Lys Asp Arg Val His Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
 420 425 430

Glu Glu Gly Ile Val Pro Gly Gly Gly Arg Pro Leu Leu Arg Cys Ile
 435 440 445
 Glu Lys Leu Glu Gly Val Glu Thr Thr Asn Glu Asp Gln Lys Leu Gly
 450 455 460
 Val Glu Ile Val Arg Arg Ala Leu Arg Met Pro Cys Met Thr Ile Ala
 465 470 475 480
 Lys Asn Ala Gly Val Asp Gly Ala Met Val Val Ala Lys Val Glu Asn
 485 490 495
 Gln Ala Gly Asp Tyr Gly Tyr Asp Ala Lys Gly Glu Tyr Gly Asn Leu
 500 505 510
 Ile Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala Ile
 515 520 525
 Thr Asp Ala Ser Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Ala Val
 530 535 540
 Val Thr Glu Ile Pro Lys Glu Asp Gly Ala Pro Ala Met Pro Gly Met
 545 550 555 560
 Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Met
 565 570 575

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg
 1 5 10 15
 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
 20 25 30
 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
 35 40 45
 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
 50 55 60
 Glu Gln Gly Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
 65 70 75 80
 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys

85										90					95				
Leu	Val	Gln	Asp	Val	Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly				
			100						105					110					
Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe				
			115					120					125						
Glu	Lys	Ile	Ser	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val				
	130					135						140							
Met	Leu	Ala	Val	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys				
145					150					155					160				
Pro	Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala				
				165					170					175					
Asn	Gly	Asp	Lys	Glu	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	Lys				
			180					185					190						
Val	Gly	Arg	Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	Leu	Asn				
		195					200					205							
Asp	Glu	Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	Gly	Tyr	Ile				
	210					215					220								
Ser	Pro	Tyr	Phe	Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	Cys	Glu	Phe	Gln				
225					230					235					240				
Asp	Ala	Tyr	Val	Leu	Leu	Ser	Glu	Lys	Lys	Ile	Ser	Ser	Ile	Gln	Ser				
				245					250					255					
Ile	Val	Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	His	Arg	Lys	Pro	Leu	Val				
			260					265					270						
Ile	Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	Ala	Leu	Ser	Thr	Leu	Val	Leu				
		275					280						285						
Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	Val	Val	Ala	Val	Lys	Ala	Pro	Gly				
	290					295					300								
Phe	Gly	Asp	Asn	Arg	Lys	Asn	Gln	Leu	Lys	Asp	Met	Ala	Ile	Ala	Thr				
305					310					315				320					
Gly	Gly	Ala	Val	Phe	Gly	Glu	Glu	Gly	Leu	Thr	Leu	Asn	Leu	Glu	Asp				
				325					330					335					
Val	Gln	Pro	His	Asp	Leu	Gly	Lys	Val	Gly	Glu	Val	Ile	Val	Thr	Lys				
			340					345					350						
Asp	Asp	Ala	Met	Leu	Leu	Lys	Gly	Lys	Gly	Asp	Lys	Ala	Gln	Ile	Glu				
		355					360					365							
Lys	Arg	Ile	Gln	Glu	Ile	Ile	Glu	Gln	Leu	Asp	Val	Thr	Thr	Ser	Glu				
	370					375					380								
Tyr	Glu	Lys	Glu	Lys	Leu	Asn	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Asp	Gly				
385					390					395				400					

G

Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
 405 410 415
 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
 420 425 430
 Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
 435 440 445
 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
 450 455 460
 Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
 465 470 475 480
 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
 485 490 495
 Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
 500 505 510
 Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
 515 520 525
 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
 530 535 540
 Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
 545 550 555 560
 Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
 565 570

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Tyr Arg Phe Ala Ser Asn Leu Ala Ser Lys Ala Arg Ile Ala Gln
 1 5 10 15
 Asn Ala Arg Gln Val Ser Ser Arg Met Ser Trp Ser Arg Asn Tyr Ala
 20 25 30
 Ala Lys Glu Ile Lys Phe Gly Val Glu Ala Arg Ala Leu Met Leu Lys
 35 40 45
 Gly Val Glu Asp Leu Ala Asp Ala Val Lys Val Thr Met Gly Pro Lys

50 55 60
 Gly Arg Asn Val Val Ile Glu Gln Ser Trp Gly Ala Pro Lys Val Thr
 65 70 75 80
 Lys Asp Gly Val Thr Val Ala Lys Ser Ile Glu Phe Lys Asp Lys Ile
 85 90 95
 Lys Asn Val Gly Ala Ser Leu Val Lys Gln Val Ala Asn Ala Thr Asn
 100 105 110
 Asp Val Ala Gly Asp Gly Thr Thr Cys Ala Thr Val Leu Thr Arg Ala
 115 120 125
 Ile Phe Ala Glu Gly Cys Lys Ser Val Ala Ala Gly Met Asn Ala Met
 130 135 140
 Asp Leu Arg Arg Gly Ile Ser Met Ala Val Asp Ala Val Val Thr Asn
 145 150 155 160
 Leu Lys Ser Lys Ala Arg Met Ile Ser Thr Ser Glu Glu Ile Ala Gln
 165 170 175
 Val Gly Thr Ile Ser Ala Asn Gly Glu Arg Glu Ile Gly Glu Leu Ile
 180 185 190
 Ala Lys Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr Ile Gln
 195 200 205
 Asp Gly Lys Thr Leu Phe Asn Glu Leu Glu Val Val Glu Gly Met Lys
 210 215 220
 Leu Asp Arg Gly Tyr Thr Ser Pro Tyr Phe Ile Thr Asn Gln Lys Thr
 225 230 235 240
 Gln Lys Cys Glu Leu Asp Asp Pro Leu Ile Leu Ile His Glu Lys Lys
 245 250 255
 Ile Ser Ser Ile Asn Ser Ile Val Lys Val Leu Glu Leu Ala Leu Lys
 260 265 270
 Arg Gln Arg Pro Leu Leu Ile Val Ser Glu Asp Val Glu Ser Asp Ala
 275 280 285
 Leu Ala Thr Leu Ile Leu Asn Lys Leu Arg Ala Gly Ile Lys Val Cys
 290 295 300
 Ala Ile Lys Ala Pro Gly Phe Gly Glu Asn Arg Lys Ala Asn Leu Gln
 305 310 315 320
 Asp Leu Ala Ala Leu Thr Gly Gly Glu Val Ile Thr Asp Glu Leu Gly
 325 330 335
 Met Asn Leu Glu Lys Val Asp Leu Ser Met Leu Gly Thr Cys Lys Lys
 340 345 350
 Val Thr Val Ser Lys Asp Asp Thr Val Ile Leu Asp Gly Ala Gly Asp
 355 360 365

Lys Lys Gly Ile Glu Glu Arg Cys Glu Gln Ile Arg Ser Ala Ile Glu
 370 375 380
 Leu Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala
 385 390 395 400
 Lys Leu Ser Gly Gly Val Ala Val Leu Lys Ile Gly Gly Ala Ser Glu
 405 410 415
 Ala Glu Val Gly Glu Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala
 420 425 430
 Thr Lys Ala Ala Val Glu Glu Gly Ile Leu Pro Gly Gly Gly Val Ala
 435 440 445
 Leu Leu Tyr Ala Ala Arg Glu Leu Glu Lys Leu Pro Thr Ala Asn Phe
 450 455 460
 Asp Gln Lys Ile Gly Val Gln Ile Ile Gln Asn Ala Leu Lys Thr Pro
 465 470 475 480
 Val Tyr Thr Ile Ala Ser Asn Ala Gly Val Glu Gly Ala Val Ile Val
 485 490 495
 Gly Lys Leu Leu Glu Gln Asp Asn Pro Asp Leu Gly Tyr Asp Ala Ala
 500 505 510
 Lys Gly Glu Tyr Val Asp Met Val Lys Ala Gly Ile Ile Asp Pro Leu
 515 520 525
 Lys Val Ile Arg Thr Ala Leu Val Asp Ala Ala Ser Val Ser Ser Leu
 530 535 540
 Leu Thr Thr Thr Glu Ala Val Val Val Asp Leu Pro Lys Asp Glu Ser
 545 550 555 560
 Glu Ser Gly Ala Ala Gly Gly Gly Met Gly Gly Met Val Val Met Asp
 565 570 575
 Tyr

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Tyr Arg Ala Ala Ala Ser Leu Ala Ser Lys Ala Arg Gln Ala Gly

1	5	10	15
Ser Ser Ser Ala Ala Arg Gln Val Gly Ser Arg Leu Ala Trp Ser Arg	20	25	30
Asn Tyr Ala Ala Lys Asp Ile Lys Phe Gly Val Glu Ala Arg Ala Leu	35	40	45
Met Leu Arg Gly Val Glu Glu Leu Ala Asp Ala Val Lys Val Thr Met	50	55	60
Gly Pro Lys Gly Arg Asn Val Val Ile Glu Gln Ser Phe Gly Ala Pro	65	70	80
Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Glu Phe Lys	85	90	95
Asp Arg Val Lys Asn Val Gly Ala Ser Leu Val Lys Gln Val Ala Asn	100	105	110
Ala Thr Asn Asp Asn Ala Gly Asp Gly Thr Thr Cys Ala Thr Val Leu	115	120	125
Thr Lys Ala Ile Phe Thr Glu Gly Cys Lys Ser Val Ala Ala Gly Met	130	135	140
Asn Ala Met Asp Leu Arg Arg Gly Ile Ser Met Ala Val Asp Ala Val	145	150	155
Val Thr Asn Leu Lys Gly Met Ala Arg Met Ile Ser Thr Ser Glu Glu	165	170	175
Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Gly Glu Arg Glu Ile Gly	180	185	190
Glu Leu Ile Ala Lys Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile	195	200	205
Thr Ile Ala Asp Gly Asn Thr Leu Tyr Asn Glu Leu Glu Val Val Glu	210	215	220
Gly Met Lys Leu Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asn	225	230	235
Ser Lys Ala Gln Lys Cys Glu Pro Glu Asp Pro Leu Ile Leu Ile His	245	250	255
Asp Arg Lys Val Thr Asn Met His Ala Val Val Lys Val Leu Glu Met	260	265	270
Ala Leu Lys Lys Gln Arg Pro Leu Leu Ile Val Ala Glu Asp Val Glu	275	280	285
Ser Glu Ala Leu Gly Thr Leu Ile Ile Asn Lys Leu Arg Ala Gly Ile	290	295	300
Lys Val Cys Ala Val Lys Ala Pro Gly Phe Gly Glu Asn Arg Lys Ala	305	310	315
			320

Asn Leu Gln Asp Leu Ala Ile Leu Thr Gly Gly Glu Val Ile Thr Glu
 325 330 335
 Glu Leu Gly Met Asn Leu Glu Asn Val Glu Pro His Met Leu Gly Ser
 340 345 350
 Cys Lys Lys Val Thr Val Ser Lys Asp Asp Thr Val Ile Leu Asp Gly
 355 360 365
 Ala Gly Asp Lys Lys Ser Ile Glu Glu Arg Ala Asp Gln Ile Arg Ser
 370 375 380
 Ala Val Glu Asn Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu
 385 390 395 400
 Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Leu Lys Ile Gly Gly
 405 410 415
 Ala Ser Glu Ala Glu Val Gly Glu Lys Lys Asp Arg Val Thr Asp Ala
 420 425 430
 Leu Asn Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly
 435 440 445
 Gly Val Ala Leu Leu Tyr Ala Ser Lys Glu Leu Asp Lys Leu Gln Thr
 450 455 460
 Ala Asn Phe Asp Gln Lys Ile Gly Val Gln Ile Ile Gln Asn Ala Leu
 465 470 475 480
 Lys Thr Pro Val His Thr Ile Ala Ser Asn Ala Gly Val Glu Gly Ala
 485 490 495
 Val Val Val Gly Lys Leu Leu Glu Gln Gly Asn Thr Asp Leu Gly Tyr
 500 505 510
 Asp Ala Ala Lys Asp Glu Tyr Val Asp Met Val Lys Ala Gly Ile Ile
 515 520 525
 Asp Pro Leu Lys Val Ile Arg Thr Ala Leu Val Asp Ala Ala Ser Val
 530 535 540
 Ser Ser Leu Met Thr Thr Thr Glu Ser Ile Ile Val Glu Ile Pro Lys
 545 550 555 560
 Glu Glu Ala Pro Ala Pro Ala Met Gly Gly Met Gly Gly Met Asp Tyr
 565 570 575

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ala Ser Thr Asn Ala Leu Ser Ser Thr Ser Ile Leu Arg Ser Pro
1 5 10 15

Thr Asn Gln Ala Gln Thr Ser Leu Ser Lys Lys Val Lys Gln His Gly
20 25 30

Arg Val Asn Phe Arg Gln Lys Pro Asn Arg Phe Val Val Lys Ala Ala
35 40 45

Ala Lys Asp Ile Ala Phe Asp Gln His Ser Arg Ser Ala Met Gln Ala
50 55 60

Gly Ile Asp Lys Leu Ala Asp Ala Val Gly Leu Thr Leu Gly Pro Arg
65 70 75 80

Gly Arg Asn Val Val Leu Asp Glu Phe Gly Ser Pro Lys Val Val Asn
85 90 95

Asp Gly Val Thr Ile Ala Arg Ala Ile Glu Leu Pro Asp Pro Met Glu
100 105 110

Asn Ala Gly Ala Ala Leu Ile Arg Glu Val Ala Ser Lys Thr Asn Asp
115 120 125

Ser Ala Gly Asp Gly Thr Thr Thr Ala Ser Ile Leu Ala Arg Glu Ile
130 135 140

Ile Lys Leu Gly Leu Leu Asn Val Thr Ser Gly Ala Asn Pro Val Ser
145 150 155 160

Ile Lys Lys Gly Ile Asp Lys Thr Val Ala Ala Leu Val Glu Glu Leu
165 170 175

Glu Lys Leu Ala Arg Pro Val Lys Gly Gly Asp Asp Ile Lys Ala Val
180 185 190

Ala Thr Ile Ser Ala Gly Asn Asp Glu Leu Ile Gly Lys Met Ile Ala
195 200 205

Glu Ala Ile Asp Lys Val Gly Pro Asp Gly Val Leu Ser Ile Glu Ser
210 215 220

Ser Asn Ser Phe Glu Thr Thr Val Glu Val Glu Glu Gly Met Glu Ile
225 230 235 240

Asp Arg Gly Tyr Ile Ser Pro Gln Phe Val Thr Asn Pro Glu Lys Ser
245 250 255

Ile Val Glu Phe Glu Asn Ala Arg Val Leu Ile Thr Asp Gln Lys Ile
260 265 270

Ser Ala Ile Lys Asp Ile Ile Pro Leu Leu Glu Lys Thr Thr Gln Leu

275 280 285
 Arg Ala Pro Leu Leu Ile Ile Ser Glu Asp Ile Thr Gly Glu Ala Leu
 290 295 300
 Ala Thr Leu Val Val Asn Lys Leu Arg Gly Ile Leu Asn Val Ala Ala
 305 310 315 320
 Ile Lys Ala Pro Gly Phe Gly Glu Arg Arg Lys Ala Leu Leu Gln Asp
 325 330 335
 Ile Ala Ile Leu Thr Gly Ala Glu Phe Gln Ala Ser Asp Leu Gly Leu
 340 345 350
 Leu Val Glu Asn Thr Thr Ile Glu Gln Leu Gly Leu Ala Arg Lys Val
 355 360 365
 Thr Ile Ser Lys Asp Ser Thr Thr Ile Ile Ala Asp Ala Ala Ser Lys
 370 375 380
 Asp Glu Leu Gln Ser Arg Val Ala Gln Leu Lys Lys Glu Leu Ser Glu
 385 390 395 400
 Thr Asp Ser Ile Tyr Asp Ser Glu Lys Leu Ala Glu Arg Ile Ala Lys
 405 410 415
 Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu Thr
 420 425 430
 Glu Leu Glu Asp Arg Lys Leu Arg Ile Glu Asp Ala Lys Asn Ala Thr
 435 440 445
 Phe Ala Ala Ile Glu Glu Gly Ile Val Pro Gly Gly Gly Thr Ala Leu
 450 455 460
 Val His Leu Ser Gly Tyr Val Pro Ala Ile Lys Glu Lys Leu Glu Asp
 465 470 475 480
 Ala Asp Glu Arg Leu Gly Ala Asp Ile Val Gln Lys Ala Leu Val Ala
 485 490 495
 Pro Ala Ala Leu Ile Ala Gln Asn Ala Gly Ile Glu Gly Glu Val Val
 500 505 510
 Val Glu Lys Ile Lys Asn Gly Glu Trp Glu Val Gly Tyr Asn Ala Met
 515 520 525
 Thr Asp Thr Tyr Glu Asn Leu Val Glu Ser Gly Val Ile Asp Pro Ala
 530 535 540
 Lys Val Thr Arg Cys Ala Leu Gln Asn Ala Ala Ser Val Ala Gly Met
 545 550 555 560
 Val Leu Thr Thr Gln Ala Ile Val Val Glu Lys Pro Lys Pro Lys Ala
 565 570 575
 Ala Val Ala Ala Ala Pro Gln Gly Leu Thr Ile
 580 585

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Lys Asp Ile Lys Phe Gly Glu Glu Ala Arg Arg Ala Met Leu
1 5 10 15

Arg Gly Val Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro
20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Ser Phe Gly Ala Pro Thr Ile
35 40 45

Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Glu Asp Lys
50 55 60

Phe Glu Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr
65 70 75 80

Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
85 90 95

Ala Ile Val Lys Glu Gly Leu Lys Asn Val Ala Ala Gly Ala Asn Pro
100 105 110

Met Asp Leu Arg Arg Gly Ile Asp Lys Ala Val Asp Ala Val Val Glu
115 120 125

Glu Leu Lys Ala Ile Ala Lys Pro Val Glu Thr Lys Glu Glu Ile Ala
130 135 140

Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Glu Glu Ile Gly Glu Leu
145 150 155 160

Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr Val
165 170 175

Glu Glu Gly Lys Thr Leu Glu Thr Glu Leu Glu Val Val Glu Gly Met
180 185 190

Gln Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asp Ser Glu
195 200 205

Lys Gln Lys Ala Glu Leu Glu Asp Pro Leu Ile Leu Leu Thr Asp Lys
210 215 220

Lys Ile Ser Asn Ile Gln Asp Leu Leu Pro Val Leu Glu Glu Val Ala

225 230 235 240
 Gln Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu
 245 250 255
 Ala Leu Ala Thr Leu Val Val Asn Lys Leu Arg Gly Thr Leu Lys Val
 260 265 270
 Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu
 275 280 285
 Gln Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu
 290 295 300
 Gly Leu Ser Leu Glu Asp Ala Thr Leu Glu Asp Leu Gly Gln Ala Lys
 305 310 315 320
 Lys Val Val Val Thr Lys Asp Asp Thr Thr Ile Val Asp Gly Ala Gly
 325 330 335
 Asp Ala Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Ser Gln Ile Glu
 340 345 350
 Glu Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala
 355 360 365
 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu
 370 375 380
 Val Glu Leu Lys Glu Arg Lys Asp Arg Val Glu Asp Ala Leu Asn Ala
 385 390 395 400
 Thr Arg Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Val Ala
 405 410 415
 Leu Leu Arg Ala Ala Pro Ala Leu Asp Lys Leu Lys Thr Glu Asn Gly
 420 425 430
 Asp Glu Ala Thr Gly Val Asn Ile Val Leu Arg Ala Leu Glu Ala Pro
 435 440 445
 Leu Arg Gln Ile Ala Glu Asn Ala Gly Leu Glu Gly Ser Val Val Val
 450 455 460
 Glu Lys Val Lys Asn Ser Glu Ala Gly Gly Tyr Asn Ala Ala Thr Gly
 465 470 475 480
 Glu Tyr Val Asp Met Ile Ala Ala Gly Ile Ile Asp Pro Thr Lys Val
 485 490 495
 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Met Leu
 500 505 510
 Thr Thr Glu Ala Val Val Val Asp Lys Pro Glu Lys Glu Ala Ala Pro
 515 520 525
 Ala Gly Met Pro Gly Met Met Gly Gly Met Gly Gly Met Gly Gly Met
 530 535 540

Met
545

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CATATGGCNG CNAAGAYGT AAAA

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TGATCACATC ATNCCNCCCA TNCC

24

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CATATGGCAA AAGAAATHAA RTTY

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGATCANCCN CCCATNCCNC CCAT

24

(2) INFORMATION FOR SEQ ID NO:39:


- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTAAAACGAC GGCCAG

16

(2) INFORMATION FOR SEQ ID NO:40:

- 
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAGGAAACAG CTATGAC

17

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAACCATCA CGAAAGA

17

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGGGTCACT TTGGTTG

17

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTACTAATGA CGGGGTA

17

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTACCAATGA CGGTGTG

17

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAGGGTCAA TGATTCC

17

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTGGATCAA TGATACC

17

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCGTACCGTG CTCTGAC

17

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACCACGTTTC AGATCCA

17

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GACAGTTTCG CGGCAAC

17

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTCAGAACGA AGATCAG

17

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTATGCAGT TCGACCG

17

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCGTGTTGGT CAAATCC

17

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGTAACTACG GTTACAA

17

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

C (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAGGCCACTT CTTTCAC

17

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGCTTCCAGC ACTGGCA

17

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AACTTCAGTC GCAGCAC

17

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCTTGAAAGC CATTGCT

17

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCTACACGTG CAGCCGT

17

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCTGCAACAG GTGAGTG

17

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCATGAACAA TGGCTTG

17

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACGAAGCACA ATGTTAC

17

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATCACTAAAG ATGGTGT

17

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAGTTGCCG CAGCAGT

17

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTACTCGTG CAGCTGT

17

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTTCTCCGTG CTTTGGA

17

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCACCTGCTG TGACGTT

17

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCTTCGATGG TGATGAC

17

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGCAAGAGCT GTTCCGC

17

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGAGCCAGT ACGGTTG

17

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTACTGCAGA GCGGAAC

17

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACCGTCTTCA ACGGTGA

17

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTTATCATTG CTGAAGA

17

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACGGTACCGC CGGTCAG

17

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TCTTCTACCG CAGCACG

17

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTCTTGATTA TTGCGGA

17

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTGTTCAAAA CAAGAGT

17

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGGGCCAGG CTAAACG

17

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGACTGAAGT TGAAATG

17

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GCTGTTGAAG AACTGAA

17

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTCTTCAACG GTGATCA

17

(2) INFORMATION FOR SEQ ID NO:78:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGATTATTGT AGAAGGT

17

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTTGATAACC GCAACAC

17

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

C
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TCCAAAGCAC GGAGAAC

17

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTGTCAAACA TCCAAGA

17

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCTTCGATGG TAATCAC

17

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCAATAATGA GTAATGG

17

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACAGTAATTG TTGAAGG

17

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAGTGCAATA CGGTTAG

17

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCTTCCAGA ACCGGCA

17

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGATCATCG CTGAAGA

17

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ACGGTTATTG TAGAAG

16
